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### (54) Modified phytases

(57) The present invention is directed to a process for the production of a modified phytase with improved activity properties characterized therein that the following steps are effected:

a) the three dimensional structure of the phytase to be modified and, optionally of another phytase with activity properties which are more favorable than the ones of the phytase to be modified is/are computer modelled on the basis of the three dimensional structure of the phytase of *Aspergillus niger*;

b) the structure of the active sites of the phytase to be modified and of the phytase with the more favorable activity properties are compared and those amino acid residues in both active sites which are different are identified;

c) a DNA sequence coding for a modified phytase is constructed by changing the nucleotides coding for at least one of the amino acids by which both active sides differ;

d) integrating such a DNA sequence into a vector

capable of expression in a suitable host cell;

e) transforming a suitable host cell by the DNA sequence of c) or the vector of d), growing said host cell under suitable growth conditions and isolating the modified phytase from the host cell or the culture medium by methods known in the state of the art.

The present invention is also directed to phytases obtainable or obtained by such a process.

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**Description**

[0001] Phytases (*myo*-inositol hexakisphosphate phosphohydrolases; EC 3.1.3.8) are enzymes that hydrolyze phytate (*myo*-inositol hexakisphosphate) to *myo*-inositol and inorganic phosphate and are known to be valuable feed additives.

[0002] A phytase was first described in rice bran in 1907 [Suzuki et al., Bull. Coll. Agr. Tokio Imp. Univ. 7, 495 (1907)] and phytases from *Aspergillus* species in 1911 [Dox and Golden, J. Biol. Chem. 10, 183-186 (1911)]. Phytases have also been found in wheat bran, plant seeds, animal intestines and in microorganisms [Howsen and Davis, Enzyme Microb. Technol. 5, 377-382 (1983), Lambrechts et al., Biotech. Lett. 14, 61-66 (1992), Shieh and Ware, Appl. Microbiol. 16, 1348-1351 (1968)].

[0003] The cloning and expression of the phytase from *Aspergillus niger* (ficum) has been described by Van Hartingsveldt et al., in Gene, 127, 87-94 (1993) and in European Patent Application, Publication No. (EP) 420 358 and from *Aspergillus niger* var. awamori by Piddington et al., in Gene 133, 55-62 (1993).

[0004] Cloning, expression and purification of phytases with improved properties have been disclosed in EP 684 313. However, since there is a still ongoing need for further improved phytases, especially with respect to the activity properties, it is an object of the present invention to provide the following:

i) A process for the production of a modified phytase with improved activity properties characterized therein that the following steps are effected:

a) the three dimensional structure of the phytase to be modified and, optionally of another phytase with activity properties which are more favorable than the ones of the phytase to be modified is/are computer modelled on the basis of the three dimensional structure of the phytase of *Aspergillus niger* (ficum);

b) the structure of the active sites of the phytase to be modified and of the phytase with the more favorable activity properties are compared and those amino acid residues in both active sites which are different are identified;

c) a DNA sequence coding for a modified phytase is constructed by changing the nucleotides coding for at least one of the amino acids by which both active sites differ;

d) integrating such a DNA sequence into a vector capable of expression in a suitable host cell;

e) transforming a suitable host cell by the DNA sequence of c) or the vector of d), growing said host cell under suitable growth conditions and isolating the modified phytase from the host cell or the culture medium by methods known in the state of the art; or

ii) a process as described under i) wherein the phytase to be modified is of eukaryotic, preferably fungal, more preferably *Aspergillus*, e.g. *Aspergillus fumigatus* origin; or

iii) a process as described under i) or ii) wherein the phytase with more favorable activity properties is of eukaryotic, preferably fungal, more preferably *Aspergillus*, e.g. *Aspergillus niger* or *Aspergillus terreus* (*Aspergillus terreus* CBS 116.46 or 9A1) origin; or

iv) a process as described under i), ii) or iii) wherein the phytase to be modified is a phytase of *Aspergillus fumigatus* and the phytase with the more favorable activity properties is the *Aspergillus terreus* phytase or the phytase of *Aspergillus niger*.

[0005] In this context it should be mentioned that another possibility of producing phytases with improved properties is by isolating phytases from the same organism, like for example the *Aspergillus* ficuum, but different strains which can be found in nature and have been deposited by any of the known depositary authorities. Their amino acid sequences can be determined by cloning their corresponding DNA sequences by methods as described, e.g. in European Patent Application No. (EP) 684 313. Once such sequences have been defined they can be modeled on the basis of the three-dimensional structure of the *A. niger* phytase and the active sites of both sequences can be compared to find out whether such phytase should have improved activity properties (see Example 8) or both active site sequences can be compared directly and then tested for increased and/or improved activity by the assays described in the present application.

[0006] It is furthermore an object of the present invention to provide a modified phytase which is obtainable by a proc-

ess as described above.

**[0007]** It is in general an object of the present invention to provide a phytase which has been modified in a way that its activity property is more favorable than the one of the non-modified phytase, specifically such a phytase characterized therein that the amino acid sequence of the non-modified phytase has been changed by deletion, substitution and/or addition of one or more amino acids, more specifically such a phytase wherein changes have been made at at least one position which is homologous to one of the following positions of the amino acid sequence of the phytase of *Aspergillus (A.) niger* (see Fig.1): 27, 66, 71, 103, 140, 141, 188, 205, 234, 235, 238, 274, 277, 282, 340 and/or 424, preferably 27, 66, 140, 205, 274, 277, 282 and/or 340, and even more specifically such a phytase which is the phytase of eukaryotic, preferably fungal, more preferably *Aspergillus* and most preferably *Aspergillus fumigatus*, origin.

**[0008]** It is furthermore an object of the present invention to provide such a phytase wherein at position 27 or at least at position 27 a change occurs, preferably a phytase wherein the amino acid at position 27 is replaced by one selected from one of the following groups:

- 15 a) Ala, Val, Leu, Ile; or
- b) Thr or
- c) Asn; and furthermore such a phytase wherein in addition to position 27 a change occurs also at position 66 or wherein in addition to position 27 a change occurs also at position 140 and/or at positions 274 and/or 277.

**[0009]** It is also an object of the present invention to provide a phytase as specified above which is characterized by 20 at least one of the following mutations: Q27L, Q27N, Q27T, Q27I, Q27V, Q27A, Q27G, S66D, S140Y, D141G, A205E, Q274L, G277D, G277K Y282H and/or N340S.

**[0010]** It is furthermore an object of the present invention to provide phytase muteins which are resistant against degradation by proteases of fungal, preferably *Aspergillus* and most preferably *Aspergillus niger* (ficuum) origin. Such muteins are characterized therein that at least at one of the following positions (which refers to the homologous position 25 in the amino acid sequence of *A. niger*), namely position 130 or 129 and 130, preferably of the *Aspergillus fumigatus* or 167, 168 preferably of the *A. nidulans* phytase amino acid sequence, the amino acid which is present in the wild type sequence has been replaced against another amino acid which is known to change the protease sensitivity, e.g. in the case of *A. fumigatus* at position 130 from "S" to "N" and at position 129 from "R" to "L" and in case of *A. nidulans* at 30 position 167 from "K" to "G" and at position 168 from R to Q. Such positions can be also combined with those providing for improved activity properties.

**[0011]** In this context "improved activity property" means any type of improvement of the activity of the mutated phytase as compared to the non mutated. This could mean for example a higher specific activity, preferably at least two fold or more preferably at least 3 to 4 fold higher in an assay known in the state of the art to measure phytase activity, see e.g. in EP 684 313 or described in the examples of the present application. Furthermore this could mean a different 35 substrate specificity determined in an assay known in the state of the art or as described e.g. in the specific examples of the present invention. This could also mean a maximum of the specific activity at a different more favorable pH or a broad pH optimum ("improved pH profile") determined by an assay as known in the state of the art or as described e.g. in the examples. Finally this could also mean any combination of such properties.

**[0012]** "Homologous" in the context of the present invention means the best fit of the primary, preferably also secondary and most preferably also tertiary structure of the phytase to be modified and the phytase of *Aspergillus niger*. How 40 such best fit can be obtained is described in detail in Example 1 of the present invention. Figure 1 gives an example of such best fit for the phytase amino acid sequences of *Aspergillus fumigatus* and *Aspergillus terreus* aligned on the basis of the *Aspergillus niger* amino acid sequence which latter sequence is also used as the reference to which the positions of the other sequences, e.g. the ones named before, are referred to. Furthermore the modified *Aspergillus fumigatus* 45 phytase with the Q27L mutation, means nothing else than the phytase of *Aspergillus fumigatus* wherein at position 27 according to the assignment as defined above (which is in fact position 23 of the *Aspergillus fumigatus* amino acid sequence) the naturally occurring glutamine ("Q" refers to the standard UPAC one letter amino acid code) has been replaced by leucine ("L"). All muteins of the present invention are designated in this way independent from whether they are protease resistant muteins or muteins with improved activity properties.

**[0013]** It is furthermore an object of the present invention to provide a DNA-sequence comprising a DNA sequence 50 coding for a phytase as described above, a vector, preferably an expression vector, comprising such a DNA sequence, a host cell which has been transformed by such a DNA sequence or vector, a process for the preparation of a phytase of the present invention wherein the host cell as described before is cultured under suitable culture conditions and the phytase is isolated from such host cell or the culture medium by methods known in the art, and a food or feed composition comprising a phytase of the present invention.

**[0014]** In this context it should be noted that it is also an object of the present invention to provide a DNA sequence 55 which codes for a phytase carrying at least one of the specific mutations of the present invention and which hybridizes under standard conditions with the DNA sequences of the specific modified phytases of the present invention or a DNA

sequence which, because of the degeneracy of the genetic code does not hybridize but which codes for a polypeptide with exactly the same amino acid sequence as the one encoded by the DNA sequence to which it does not hybridize or a DNA sequence which is a fragment of such DNA sequences which maintains the activity properties of the polypeptide of which it is a fragment.

- 5 [0015] "Standard conditions" for hybridization mean in the context the conditions which are generally used by a man skilled in the art to detect specific hybridization signals and which are described, e.g. by Sambrook et al., "Molecular Cloning", second edition, Cold Spring Harbor Laboratory Press 1989, New York, or preferably so called stringent hybridization and non-stringent washing conditions or more preferably so called stringent hybridization and stringent washing conditions a man skilled in the art is familiar with and which are described, e.g. in Sambrook et al. (s.a.).
- 10 [0016] It is furthermore an object of the present invention to provide a DNA sequence which can be obtained by the so called polymerase chain reaction method ("PCR") by PCR primers designed on the basis of the specifically described DNA sequences of the present invention. It is understood that the so obtained DNA sequences code for phytases with at least the same mutation as the ones from which they are designed and show comparable activity properties.
- 15 [0017] The principles of the polymerase chain reaction (PCR) method are outlined e.g. by White et al., Trends in Genetics, 5, 185-189 (1989), whereas improved methods are described e.g. in Innis et al. [PCR Protocols: A guide to Methods and Applications, Academic Press, Inc. (1990)].
- [0018] DNA sequences of the present invention can be constructed starting from genomic or cDNA sequences coding for phytases known in the state of the art [for sequence information see references mentioned above, e.g. EP 684 313 or sequence data bases, for example like Genbank (Intelligenetics, California, USA), European Bioinformatics Institute (Hinstone Hall, Cambridge, GB), NBRF (Georgetown University, Medical Centre, Washington DC, USA) and Vecbase (University of Wisconsin, Biotechnology Centre, Madison, Wisconsin, USA) or disclosed in the figures by methods of in vitro mutagenesis [see e.g. Sambrook et al., Molecular Cloning, Cold Spring Harbor Laboratory Press, New York]. A widely used strategy for such "site directed mutagenesis", as originally outlined by Hurchinson and Edgell [J. Virol. 8, 181 (1971)], involves the annealing of a synthetic oligonucleotide carrying the desired nucleotide substitution to a target region of a single-stranded DNA sequence wherein the mutation should be introduced [for review see Smith, Annu. Rev. Genet. 19, 423 (1985) and for improved methods see references 2-6 in Stanssen et al., Nucl. Acid Res., 17, 4441-4454 (1989)]. Another possibility of mutating a given DNA sequence which is also preferred for the practice of the present invention is the mutagenesis by using the polymerase chain reaction (PCR). DNA as starting material can be isolated by methods known in the art and described e.g. in Sambrook et al. (Molecular Cloning) from the respective strains. For strain information see, e.g. EP 684 313 or any depositary authority indicated below. Aspergillus niger [ATCC 9142], Myceliophthora thermophila [ATCC 48102], Talaromyces thermophilus [ATCC 20186] and Aspergillus fumigatus [ATCC 34625] have been redeposited on March 14, 1997 according to the conditions of the Budapest Treaty at the American Type Culture Cell Collection under the following accession numbers: ATCC 74337, ATCC 74340, ATCC 74338 and ATCC 74339, respectively. It is however, understood that DNA encoding a phytase to be mutated in accordance with the present invention can also be prepared on the basis of a known DNA sequence, e.g. as shown in Fig. 6 in a synthetic manner and described e.g. in EP 747 483 by methods known in the art.
- [0019] Once complete DNA sequences of the present invention have been obtained they can be integrated into vectors by methods known in the art and described e.g. in Sambrook et al. (s.a.) to overexpress the encoded polypeptide in appropriate host systems. However, a man skilled in the art knows that also the DNA sequences themselves can be used to transform the suitable host systems of the invention to get overexpression of the encoded polypeptide. Appropriate host systems are for example fungi, like Aspergilli, e.g. Aspergillus niger [ATCC 9142] or Aspergillus ficuum [NRRL 3135] or like Trichoderma, e.g. Trichoderma reesei or yeasts, like Saccharomyces, e.g. Saccharomyces cerevisiae or Pichia, like Pichia pastoris, or Hansenula polymorpha, e.g. H. polymorpha (DSM5215). A man skilled in the art knows that such microorganisms are available from depositary authorities, e.g. the American Type Culture Collection (ATCC), the Centraalbureau voor Schimmelcultures (CBS) or the Deutsche Sammlung für Mikroorganismen und Zellkulturen GmbH (DSM) or any other depositary authority as listed in the Journal "Industrial Property" [(1991) 1, pages 29-40]. Bacteria which can be used are e.g. E. coli, Bacilli as, e.g. Bacillus subtilis or Streptomyces, e.g. Streptomyces lividans (see e.g. Anné and Mallaert in FEMS Microbiol. Letters 114, 121 (1993)). E. coli, which could be used are E. coli K12 strains e.g. M15 [described as DZ 291 by Villarejo et al. in J. Bacteriol. 120, 466-474 (1974)], HB 101 [ATCC No. 33694] or E. coli SG13009 [Gottesman et al., J. Bacteriol. 148, 265-273 (1981)].
- [0020] Vectors which can be used for expression in fungi are known in the art and described e.g. in EP 420 358, or by Cullen et al. [Bio/Technology 5, 369-376 (1987)] or Ward in Molecular Industrial Mycology, Systems and Applications for Filamentous Fungi, Marcel Dekker, New York (1991), Upshall et al. [Bio/Technology 5, 1301-1304 (1987)] Gwynne et al. [Bio/Technology 5, 71-79 (1987)], Punt et al. [J. Biotechnol. 17, 19-34 (1991)] and for yeast by Sreekrishna et al. [J. Basic Microbiol. 28, 265-278 (1988), Biochemistry 28, 4117-4125 (1989)], Hitzemann et al. [Nature 293, 717-722 (1981)] or in EP 183 070, EP 183 071, EP 248 227, EP 263 311. Suitable vectors which can be used for expression in E. coli are mentioned, e.g. by Sambrook et al. [s.a.] or by Fiers et al. in Procd. 8th Int. Biotechnology Symposium" [Soc.

Franc. de Microbiol., Paris (Durand et al., eds.), pp. 680-697 (1988)] or by Bujard et al. in Methods in Enzymology, eds. Wu and Grossmann, Academic Press, Inc. Vol. 155, 416-433 (1987) and Stüber et al. in Immunological Methods, eds. Lefkovits and Pernis, Academic Press, Inc., Vol. IV, 121-152 (1990). Vectors which could be used for expression in Bacilli are known in the art and described, e.g. in EP 405 370, Procd. Natl. Acad. Sci. USA 81, 439 (1984) by Yansura and Henner, Meth. Enzymol. 185, 199-228 (1990) or EP 207 459. Vectors which can be used for the expression in H. Polymorpha are known in the art and described, e.g. in Gellissen et al., Biotechnology 9, 291-295 (1991).

[0021] Either such vectors already carry regulatory elements, e.g. promotors, or the DNA sequences of the present invention can be engineered to contain such elements. Suitable promotor elements which can be used are known in the art and are, e.g. for *Trichoderma reesei* the cbh1- [Haarki et al., Biotechnology 7, 596-600 (1989)] or the pki1-promotor [Schindler et al., Gene 130, 271-275 (1993)], for *Aspergillus oryzae* the amy-promotor [Christensen et al., Abstr. 19th Lunteren Lectures on Molecular Genetics F23 (1987), Christensen et al., Biotechnology 6, 1419-1422 (1988), Tada et al., Mol. Gen. Genet. 229, 301 (1991)], for *Aspergillus niger* the glaA- [Cullen et al., Bio/Technology 5, 369-376 (1987), Gwynne et al., Bio/Technology 5, 713-719 (1987), Ward in Molecular Industrial Mycology, Systems and Applications for Filamentous Fungi, Marcel Dekker, New York, 83-106 (1991)], alcA- [Gwynne et al., Bio/Technology 5, 718-719 (1987)], suc1- [Boddy et al., Curr. Genet. 24, 60-66 (1993)], aphA- [MacRae et al., Gene 71, 339-348 (1988), MacRae et al., Gene 132, 193-198 (1993)], tpiA- [McKnight et al., Cell 46, 143-147 (1986), Upshall et al., Bio/Technology 5, 1301-1304 (1987)], gpda- [Punt et al., Gene 69, 49-57 (1988), Punt et al., J. Biotechnol. 17, 19-37 (1991)] and the pkiA-promotor [de Graaff et al., Curr. Genet. 22, 21-27 (1992)]. Suitable promotor elements which could be used for expression in yeast are known in the art and are, e.g. the pho5-promotor [Vogel et al., Mol. Cell. Biol., 2050-2057 (1989); Rudolf and Hinnen, Proc. Natl. Acad. Sci. 84, 1340-1344 (1987)] or the gap-promotor for expression in *Saccharomyces cerevisiae* and for *Pichia pastoris*, e.g. the aox1-promotor [Koutz et al., Yeast 5, 167-177 (1989); Sreekrishna et al., J. Basic Microbiol. 28, 265-278 (1988)], or the FMD promoter [Hollenberg et al., EPA No. 0299108] or MOX-promotor [Ledeboer et al., Nucleic Acids Res. 13, 3063-3082 (1985)] for *H. polymorpha*.

[0022] Accordingly vectors comprising DNA sequences of the present invention, preferably for the expression of said DNA sequences in bacteria or a fungal or a yeast host and such transformed bacteria or fungal or yeast hosts are also an object of the present invention.

[0023] Once such DNA sequences have been expressed in an appropriate host cell in a suitable medium the encoded phytase can be isolated either from the medium in the case the phytase is secreted into the medium or from the host organism in case such phytase is present intracellularly by methods known in the art of protein purification or described, e.g. in EP 420 358. Accordingly a process for the preparation of a polypeptide of the present invention characterized in that transformed bacteria or a host cell as described above is cultured under suitable culture conditions and the polypeptide is recovered therefrom and a polypeptide when produced by such a process or a polypeptide encoded by a DNA sequence of the present invention are also an object of the present invention.

[0024] Phytases of the present invention can be also expressed in plants according to methods as described, e.g. by Pen et al. in Bio/Technology 11, 811-814 (1994) or in EP 449 375, preferably in seeds as described, e.g. in EP 449 376.

[0025] For example, a DNA sequence encoding a phytase of the present invention can be placed under the control of regulatory sequences from the gene encoding the 12S storage protein cruciferin from *Brassica napus*. The construct is thereafter subcloned into a binary vector such as pMOG23 (in *E. coli* K-12 strain DH5 $\alpha$ , deposited at the Centraal Bureau voor Schimmelcultures, Baarn, The Netherlands under accession number CBS 102.90). This vector is introduced into *Agrobacterium tumefaciens* which contains a disarmed Ti plasmid. Bacterial cells containing this construct are co-cultivated with tissues from tobacco or *Brassica* plants, and transformed plant cells are selected by nutrient media containing antibiotics and induced to regenerate into differentiated plants on such media. The resulting plants will produce seeds that contain and express the DNA construct. Or the phytase-encoding DNA sequence can be placed under the control of regulatory sequences from the 35S promoter of Cauliflower Mosaic Virus (CaMV). The construct is thereafter subcloned into a binary vector. This vector is then introduced into *Agrobacterium tumefaciens* which contains a disarmed Ti plasmid. Bacterial cells containing this construct are cocultivated with tissues from tobacco or *Brassica* plants, and transformed plant cells are selected by nutrient media containing antibiotics and induced to regenerate into differentiated plants on such media. The resulting plants contain and express the DNA construct constitutively.

[0026] The plant or plant part containing phytase can be used directly for the preparation of a feed composition or can be extracted from plants or plant organs by methods known in the art. Accordingly it is also an object of the present invention to provide a process for the production of the phytases of the present invention in plants or plant organs, like seeds, the phytases when produced by such methods, the transformed plants and plant organs, like seeds itself.

[0027] Once obtained the polypeptides of the present invention can be characterized regarding their properties which make them useful in agriculture any assay known in the art and described e.g. by Simons et al. [Br. J. Nutr. 64, 525-540 (1990)], Schöner et al. [J. Anim. Physiol. a. Anim. Nutr. 66, 248-255 (1991)], Vogt [Arch. Geflügelk. 56, 93-98 (1992)], Jongbloed et al. [J. Anim. Sci., 70, 1159-1168 (1992)], Perney et al. [Poultry Sci. 72, 2106-2114 (1993)], Farrell et al., [J. Anim. Physiol. a. Anim. Nutr. 69, 278-283 (1993), Broz et al., [Br. Poultry Sci. 35, 273-280 (1994)] and Dünghelhoef et al. [Animal Feed Sci. Technol. 49, 1-10 (1994)] can be used.

[0028] In general the polypeptides of the present invention can be used without being limited to a specific field of application for the conversion of inositol polyphosphates, like phytate to inositol and inorganic phosphate.

[0029] Furthermore the polypeptides of the present invention can be used in a process for the preparation of compound food or feeds wherein the components of such a composition are mixed with one or more polypeptides of the present invention. Accordingly compound food or feeds comprising one or more polypeptides of the present invention are also an object of the present invention. A man skilled in the art is familiar with their process of preparation. Such compound foods or feeds can further comprise additives or components generally used for such purpose and known in the state of the art.

[0030] It is furthermore an object of the present invention to provide a process for the reduction of levels of phytate in animal manure characterized in that an animal is fed such a feed composition in an amount effective in converting phytate contained in the feedstuff to inositol and inorganic phosphate.

[0031] Before describing the present invention in more detail a short explanation of the enclosed Figures is given below.

15 **Figure Legends**

[0032]

20 **Figure 1:** Primary sequence alignment of *A. niger* (*ficum*), *A. terreus* CBS116.46 and *A. fumigatus* [ATCC 13073] phytase. Stars show identical residues within the active site and rectangles, non-identical residues within the active site.

25 **Figure 2:** pH optima curves. Specific activity of wild-type and mutant *A. fumigatus* phytases is plotted against pH of incubation. Filled squares represent *A. fumigatus* wild-type phytase; Open triangles represent *A. fumigatus* Q27L mutant; Filled circles represent *A. fumigatus* Q27L, Q274L mutant; Open squares represent *A. fumigatus* Q27L, Q274L, G277D mutant.

30 **Figure 3:** Substrate specificities of wild-type and mutant *A. fumigatus* phytases. (A) wild-type; (B) Q27L single mutant; (C) Q27L, Q274L, G277D triple mutant. The following substrates were used: (1) phytic acid; (2) p-nitrophenyl phosphate; (3) fructose-1,6-bisphosphate; (4) fructose-6-phosphate; (5) glucose-6-phosphate; (6) ribose-5-phosphate; (7)  $\alpha$ -glycerophosphate; (8)  $\beta$ -glycerophosphate; (9) 3-phosphoglycerate; (10) phosphoenolpyruvate; (11) AMP; (12) ADP; (13) ATP.

35 **Figure 4:** Complete coding sequence and encoded amino acid sequence of the *Aspergillus nidulans* phytase.

**Figure 5:** Complete coding sequence and encoded amino acid sequence of *Talaromyces thermophilus* phytase.

40 **Figure 6:** Complete coding sequence and encoded amino acid sequence of *Aspergillus fumigatus* [ATCC 13073] phytase.

45 **Figure 7:** Complete coding sequence and encoded amino acid sequence of *Aspergillus terreus* CBS 116.46 phytase.

**Figure 8:** Crystallographic data of the structure of the *Aspergillus niger* phytase.

50 **Figure 9:** Substrate specificities of wild-type and mutant *A. fumigatus* phytase (N1-N6). Substrates 1 to 13 are as indicated for Figure 3.

**Figure 10:** pH optima curves of further mutant *A. fumigatus* phytases (N1-N6). All activity values were standardized (maximum activity = 1.0).

55 **Figure 11a:** Stereo picture of the three-dimensional fold of *A. niger* (*A. ficuum*; NRRL 3135) phytase. The active site is indicated with a circle and the catalytically essential amino acid residues Arg 58 and His 59 are shown in ball-and-stick representation. This figure was prepared with the programs "MOLSCRIPT" [Kraulis, P.J., J. Appl. Cryst. 24, 946-950 (1991)] and "RASTER3D" [Merritt, E.A. & Murphy, M.E.P., Acta Cryst., 869-873 (1994)].

**Figure 11b:** Topological sketch, using the same scheme as in (a). The five disulphide bridges are shown as black

5 zigzag lines together with the sequence numbers of the cysteine residues involved. The  $\beta$ -strands are defined with the sequence numbers A: 48-58, B: 134-138, C: 173-177, D: 332-337, E: 383-391, and F: 398-403. The  $\alpha$ -helices are defined with the sequence numbers a: 66-82, b: 88-95, c: 107-123, d: 141-159, e: 193-197, f: 200-210, g: 213-223, h: 231-246, i: 257-261, j: 264-281, k: 290-305, l: 339-348, m: 423-429, and n: 439-443. The asterisk at the C-terminal end of  $\beta$ -strand A marks the location of the catalytically essential amino acid residues Arg 58 and His 59.

- 10 **Figure 12:** Stereo picture of the active site of *A. fumigatus* (ATCC 13073) phytase with a hypothetical binding mode of the substrate phytate. In this model, the bound crystal water molecules were removed and the protein atom positions were held fixed, except for small adaptations of the side chain torsion angles of Lys 68 in order to interact with the substrate. All the conserved amino acid residues Arg 58, His 59, Arg 62, Arg 142, His 338 and Asp 339 form hydrogen bonds to the scissile 3-phosphate group of phytate, as indicated with lines of small dots. His 59 is in a favorable position to make a nucleophilic attack at the scissile phosphorous, indicated with a line of larger dots, and Asp 339 is in a position to protonate the leaving group.
- 15 **Figure 13:** Construction of the basic plasmids pUC18-AfumgDNA and pUC18-AfumcDNA for site directed mutagenesis.
- 20 **Figure 14a:** Primer sets A-N used for site directed mutagenesis.
- Figure 14b:** Primer sets O-T used for site directed mutagenesis.
- 25 **Figure 15:** Construction of plasmids pgDNAT1-pgDNAT7.
- Figure 16:** Construction of plasmids pgDNAN1-pgDNAN6.
- 30 **Figure 17a:** Construction of plasmids pcT1 - pcT7.
- Figure 17b:** Construction of plasmids pcT1-AvrlI, pcT1-S66D and pcT1-S140Y-D141G
- 35 **Figure 17c:** Construction of plasmids pcDNA-N27, -T27, -I27, -V27, -A27, -G27.
- Figure 18:** Construction of plasmids pcN1- pcN6.
- 40 **Figure 19:** Plasmid pAfum-T1 for the expression of mitein T1 in *Aspergillus niger*.
- Figure 20:** pH optima curves. Specific activity of wild-type and mutant *A. fumigatus* phytases is plotted against pH of incubation. Open triangles: *A. fumigatus* [ATCC 13073] wild-type phytase; Open rhombs: *A. fumigatus* Q27G phytase; Filled squares: *A. fumigatus* Q27N phytase; Filled triangles: *A. fumigatus* Q27V phytase; Open squares: *A. fumigatus* Q27A phytase; Filled circles: *A. fumigatus* Q27I phytase; Open circles: *A. fumigatus* Q27T phytase; Dashed line: *A. fumigatus* Q27L phytase.
- 45 **Figure 21:** Substrate specificities of wild-type and mutant *A. fumigatus* [ATCC 13073] phytases. The used substrates 1-13 are the same as mentioned in Figure 3. The specific activities of the different phytases with any one of the 13 substrates tested are given in the following order (from left to right): *A. fumigatus* wild-type phytase, *A. fumigatus* Q27N phytase, *A. fumigatus* Q27T phytase, *A. fumigatus* Q27L phytase, *A. fumigatus* Q27I phytase, *A. fumigatus* Q27V phytase, *A. fumigatus* Q27A phytase, *A. fumigatus* Q27G phytase.
- 50 **Figure 22:** pH optima curves. Specific activity of wild-type and mutant *A. fumigatus* [ATCC 13073] phytases is plotted against pH of incubation. Filled rhombs: *A. fumigatus* wild-type phytase; Filled squares: *A. fumigatus* Q27L single mutant; Open circles: *A. fumigatus* Q27L-S66D double mutant; Filled triangles: *A. fumigatus* Q27L-S140Y-D141G triple mutant.
- 55 **Figure 23:** Natural variation of phytases in different isolates of *A. fumigatus* [ATCC 13073]. The predicted protein sequences are shown and compared to that of the phytase from *A. fumigatus* strain ATCC 13073. Only the amino acids which differ from those in #13073 are shown.

**Figure 24:** pH dependent specific activity of phytases isolated from two different *A. fumigatus* wildtype strains. Open squares: wild-type strain ATCC 13073; Filled circles: strain ATCC 32239.

**Figure 25:** Substrate specificities of phytases isolated from two different *A. fumigatus* wildtype strains. Black bars: wild-type strain ATCC 13073; White bars: strain ATCC 32239.

**Figure 26:** Construction of plasmids pc-S130N, pc-R129L-S130N, pc-K167G-R168Q.

#### Examples

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##### Example 1

###### Homology Modeling of *A. fumigatus* and *A. terreus* cbs116.46 phytase

15 [0033] The amino acid sequences of *A. fumigatus* [ATCC 13073] (see Figure 1) and *A. terreus* cbs116.46 phytase (see Figure 1) were compared with the sequence of *A. niger* (*ficum*) phytase (see Figure 1) for which the three-dimensional structure had been determined by X-ray crystallography. Crystallographic data are given in Figure 8.

20 [0034] A multiple amino acid sequence alignment of *A. niger* (*ficum*) phytase, *A. fumigatus* phytase and *A. terreus* cbs116.46 phytase was calculated with the program "PILEUP" (Prog. Menu for the Wisconsin Package, version 8, September 1994, Genetics Computer Group, 575 Science Drive, Madison Wisconsin, USA 53711). The three-dimensional models of *A. fumigatus* phytase and *A. terreus* cbs116.46 phytase were built by using the structure of *A. niger* (*ficum*) phytase as template and exchanging the amino acids of *A. niger* (*ficum*) phytase according to the sequence alignment to amino acids of *A. fumigatus* and *A. terreus* cbs116.46 phytases, respectively. Model construction and energy optimization were performed by using the program Moloc (Gerber and Müller, 1995). C-alpha positions were kept fixed except for new insertions/deletions and in loop regions distant from the active site.

25 [0035] Only small differences of the modelled structures to the original crystal structure could be observed in external loops. Furthermore the different substrate molecules that mainly occur on the degradation pathway of phytic acid (*myo*-inositol-hexakisphosphate) by *Pseudomonas* sp. *bacterium* phytase and, as far as determined, by *A. niger* (*ficum*) phytase (Cosgrove, 1980; Fig. 1) were constructed and forged into the active site cavity of each phytase structure. Each 30 of these substrates was oriented in a hypothetical binding mode proposed for histidine acid phosphatases (Van Etten, 1982). The scissile phosphate group was oriented towards the catalytically essential His 59 to form the covalent phosphoenzyme intermediate. The oxygen of the substrate phosphoester bond which will be protonated by Asp 339 after cleavage was orientated towards the proton donor. Conformational relaxation of the remaining structural part of the substrates as well as the surrounding active site residues was performed by energy optimization with the program 35 Moloc.

[0036] Based on the structure models the residues pointing into the active site cavity were identified. More than half (60%) of these positions were identical between these three phytases, whereas only few positions were not conserved (see Figure 1). This observation could be extended to four additional phytase sequences (*A. nidulans*, *A. terreus* 9A1, *Talaromyces thermophilus*, *Myceliophthora thermophila*).

40 [0037] The results coming from sequence alignment and structural information including favourable enzyme-substrate interactions were combined to define the positions for mutational analysis which are shown in Table 1.

#### References:

45 [0038]

Gerber, P. and Müller, K. (1995) Moloc molecular modeling software. J. Comput. Aided Mol. Des. 9, 251-268

Van Etten, R.L. (1982) Human prostatic acid phosphatase: a histidine phosphatase. Ann. NY Acad. Sci. 390, 27-50

50 Cosgrove, D.J. (1980) Inositol phosphates - their chemistry, biochemistry and physiology: studies in organic chemistry, chapter 4. Elsevier Scientific Publishing Company, Amsterdam, Oxford, New York.

#### Example 2

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##### Construction of plasmids pUC18-AfumgDNA and pUC18-AfumcDNA

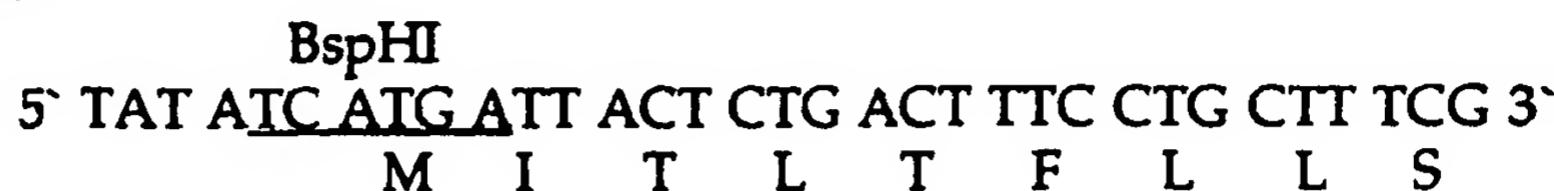
[0039] Plasmids pUC18-AfumgDNA and pUC18-AfumcDNA, the basic constructs for all the *A. fumigatus* mureins

described below were constructed as follows.

- [0040] pUC18-AfumgDNA: The genomic DNA sequence of the phytase gene of *Aspergillus fumigatus* was obtained by PCR using the "Expand™ High Fidelity PCR Kit" (Boehringer Mannheim, Mannheim, Germany) with primers #39 and #40 (designed on the basis of the genomic sequence shown in Figure 6) and genomic DNA of *Aspergillus fumigatus* [ATCC 13073] from the A. fumigatus (NIH stock 5233) genomic library in a Lambda FixII vector [Stratagene, La Jolla, CA 92037, USA; catalog No. 946055].

Primer #39:

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Primer #40:



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- [0041] The reaction mix included 10 pmol of each primer and 200 ng of template DNA. 35 rounds of amplification were done with the following cycling values: 95 °C, 1 min/56 °C, 1 min/72 °C, 90 sec. The PCR-amplified *Aspergillus fumigatus* murein genes had a new BspHI site at the ATG start codon, introduced with primer #39, which resulted in the 25 change of the second amino acid from a valine to an isoleucine. Furthermore, an EcoRV site was created with primer #40 downstream of the TGA termination codon of the gene.

[0042] The PCR fragment (approx. 1450 bp) was subsequently cloned into the SmaI site of pUC18 using the "sure clone Kit" (Boehringer Mannheim s.a.) according to the supplier's recommendations. The resulting plasmid was named pUC18-AfumgDNA.

- [0043] pUC18-AfumcDNA: This plasmid lacks the intron (small gap letters in Figure 6) of the A. fumigatus phytase gene and was constructed as outlined in Figure 13. Briefly, using primers Fum28 and Fum11 the 5' end of exon 2 was amplified by PCR (see below), digested with NcoI and EagI (new restriction site introduced with primer Fum28) and ligated together with the linker coding for exon 1 made of primers Fum26 and Fum27 into the XbaI and NcoI sites of pUC18-AfumgDNA, thereby resulting in plasmid pUC18-AfumcDNA.

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**Fum28:**

5' ATATATCGGCCGAGTGTCTGCGGCACCTAGT 3'  
EagI

**Fum11:**

10' TGAGGT~~CATCCGCACCCAGAG~~ 3'

**Fum26:**

15' CTAGAATT~~CATGGTGACTCTGACTTT~~CCTGCTTCGGCGGTATCT  
GCTTTCC 3'

**Fum27:**

20' 5' GGCCGGAAAGCAGATACGCCGCCAAAGCAGGAAAGTCAGAGTC  
ACCATGAATT 3'

25 PCR reaction to get 5' end of exon 2 of the *A. fumigatus* phytase:

2 µl	template: pUC18-AfumgDNA (20 ng)
1 µl	dNTP's-mix (Boehringer Mannheim s.a.)
30 5 µl	10x Buffer
1 µl	Taq polymerase (Boehringer Mannheim s.a.)
1.9 µl	Fum11 (=10 pmol)
2 µl	Fum28 (=10 pmol)
37.1 µl	H <sub>2</sub> O

35 [0044] In total 35 cycles with the temperature profile: 95°C for 30 sec/56°C for 30 sec/ 72°C for 45 sec were made. The amplified fragment (approx. 330 bp) was extracted once with an equal volume of phenol/chloroform (1:1). To the recovered aqueous phase 0.1 volume of 3 M sodium acetate, pH 4.8 and 2.5 volumes of ethanol were added. The mixture was centrifuged for 10 min at 12000 g and the pellet resuspended in 20 µl of H<sub>2</sub>O. Subsequently, the purified fragment was digested with Ncol and EagI and processed as outlined above.

**Example 3****Construction of muteins of the phytase of *Aspergillus fumigatus* for expression in *A. niger***

45 [0045] To construct all muteins for the expression in *A. niger*, plasmid pUC18-AfumgDNA was used as template for site-directed mutagenesis. Mutations were introduced using the "quick exchange™ site-directed mutagenesis kit" from Stratagene (La Jolla, CA, USA) following the manufacturer's protocol and using the corresponding primers (Figure 14). All mutations made are summarized in Table 1A and B wherein T1 to T7 and N1 to N6, respectively, refer to the muteins and "Mutation" to the amino acids replaced at such position. For example T5 refers to a mutein with a double mutation: L at position 27 for Q and L at position 274 for Q. The primer sets (A-H) used to introduce the corresponding mutations are shown in Figure 14a. The newly introduced amino acid is shown in bold and the subscript indicates the position in the mature *Aspergillus fumigatus* enzyme concerning to the numbering of the *A. niger* amino acid sequence. Figures 15 and 16 outline the scheme for the construction of different plasmids pgT1-pgT7 and pgN1-pgN6 encoding the muteins carrying only one mutation (T1-T4; N1-N3) or more mutations (T5-T7; N4-N6). Clones harboring the desired mutations were identified by DNA sequence analysis as known in the art. The mutated phytases were verified by complete sequencing of the genes.

Example 4Construction of muteins of the phytase of *Aspergillus fumigatus* for expression in *Saccharomyces cerevisiae*

- 5 [0046] Construction of plasmids pcT1 - pcT7 (Figure 17a) and pcN1 - pcN6 (Figure 18), respectively, encoding the muteins T1-T7 and N1-N6 for the expression in *S. cerevisiae* was basically done as outlined in Example 3. Instead of using pUC18-AfumcDNA as the basic construct to introduce the mutations, plasmid pUC18-AfumcDNA was used (Figure 13).
- 10 [0047] The plasmids pcDNA-N27, -G27, -V27, -A27, -I27 and -T27 encoding the muteins N27, G27, V27, A27, I27 and T27 were constructed as follows:
- [0048] A silent restriction site for AvrII was introduced into plasmid pcT1 by site directed mutagenesis as described in Example 3 using primer set I (Figure 14a; Figure 17b). The *A. fumigatus* phytase gene fragment AvrII/Xhol was then replaced by the linker fragment harbouring the desired mutations (Figure 17c). Each linker fragment was generated by annealing of the respective pairs of synthesized polynucleotides (Fig. 14b; sense and antisense strand; 90 ng each) for 15 3 min at 70 °C in 9 µl distilled water.
- [0049] Construction of plasmids pcT1-S66D and pcT1-S140Y-D141G encoding the *A. fumigatus* Q27L-S66D double mutant and the *A. fumigatus* Q27L-S140Y-D141G triple mutant was basically carried out as described in Example 3. Plasmid pcT1, harbouring the mutation coding for Q27L, was used as template for site directed mutagenesis together with the corresponding primer sets J and K (Figure 14a; Figure 17b).
- 20 [0050] All mutations were verified by DNA sequence analysis of the entire gene.

Example 5Expression in *Aspergillus niger*

- 25 [0051] The genes encoding the aforementioned *A. fumigatus* wild-type phytase and muteins (Fig. 16) were isolated with BspHI and EcoRV from plasmids pgDNAT1-pgDNAT7 and pgDNAN1-pgDNAN6 and ligated into the Ncol site downstream of the glucoamylase promoter of *Aspergillus niger* (*glA*A) and the EcoRV site upstream of the *Aspergillus nidulans* tryptophan C terminator (*trpC*) (Mullaney et al., 1985). The resulting expression plasmids had in addition the orotidine-5'-phosphate decarboxylase gene (*pyr4*) of *Neurospora crassa* as selection marker. Figure 19 shows an example for such an expression plasmid carrying the gene encoding mutein T1 (van den Hondel et al., 1991). The basic expression plasmid described above corresponds basically to the pGLAC vector described in example 9 of EP 684 313. Transformation of *Aspergillus niger* and expression of the muteins was done as described in EP 684 313.
- [0052] The supernatant was concentrated by way of ultrafiltration in Amicon 8400 cells (PM30 membranes) and ultra-free-15 centrifugal filter devices (Biomax-30K, Millipore).
- [0053] The concentrate (typically 1.5-5 ml) was desalting in aliquots of 1.5 ml on a Fast Desalting HR 10/10 column (Pharmacia Biotech), with 10 mM sodium acetate, pH 5.0, serving as elution buffer. The desalting *A. fumigatus* samples were directly loaded onto a 1.7 ml Poros HS/M cation exchange chromatography column (PerSeptive Biosystems, Framingham, MA, USA). *A. terreus* CBS116.46 [CBS 220.95] phytase was directly loaded onto a 1.7 ml Poros HQ/M anion exchange chromatography column. In both cases, phytase was eluted in pure form by way of a sodium chloride gradient.

## References:

- 45 [0054]

- Mullaney, E. J., J. E. Hamer, K. A. Roberti, M. M. Yelton, and W. E. Timberlake. 1985. Primary structure of the *trpC* gene from *Aspergillus nidulans*. Mol. Gen. Genet. 199:37-45.
- Van den Hondel, C. A. M. J. J., P. J. Punt, and R. F. M. van Gorcom. 1991. Heterologous gene expression in filamentous fungi. In: More gene manipulations in fungi. pp. 396-428. Bennett, J. W. and Lasure, L. L. (eds.). Academic Press Inc., San Diego, CA.

Example 6Expression in *Saccharomyces cerevisiae*

- 55 [0055] The intron less genes encoding the *A. fumigatus* wild-type phytase and the different muteins (Fig. 17/18) mentioned above were isolated from the respective plasmids pUC18-AfumcDNA, pcDNAT1 - pcDNAT7 and pcDNAN1 -

pcDNAN6 with EcoRI and EcoRV and subcloned either between the blunt ended XbaI and the EcoRI sites of plasmid pYES2 (Invitrogen, San Diego, CA, USA) or the shortened GAPFL (glyceraldehyde-3-phosphate dehydrogenase) promoter and the PHO5 terminator as described by Janes et al. (1990). Transformation of *Saccharomyces cerevisiae* strains, e.g. INVSc1 (Invitrogen, San Diego, CA, USA) was done according to Hinnen et al. (1978). Single colonies harbouring the phytase gene under the control of the GAPFL promoter were picked and cultivated in 5ml selection medium (SD -uracil) (Sherman et al., 1986) at 30° C under vigorous shaking (250 rpm) for 1 day. The preculture was then added to 500 ml YPD medium (Sherman et al., 1986) and cultivated under the same conditions. After four days cell broth was centrifuged (7000 rpm, GS3 rotor, 15 min. 5° C) and the supernatant was collected. Induction of the GAL1 promotor (plasmid pYES2 from Invitrogen, San Diego, CA, USA) was done according to the manufacturers instructions. Purification of the mureins was as described in example 5 (s.a.).

#### References:

##### [0056]

- 15 Janes, M., B. Meyhack, W. Zimmermann and A. Hinnen. 1990. The influence of GAP promoter variants on hirudine production, average plasmid copy number and cell growth in *Saccharomyces cerevisiae*. *Curr. Genet.* 18: 97-103
- 20 Hinnen, A., J.B. Hicks and G.R. Fink. 1978. Proc. Natl. Acad. Sci. USA 75: 1929-1933
- Sheman, J.P., Fink, G.R. and Hicks, J.B. (1986). Laboratory Course Manual for Methods in Yeast Genetics. Cold Spring Harbor University Press.

#### Example 7

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##### Determination of phytase activity and substrate specificity

[0057] Phytase activity was measured in an assay mixture containing 0.5% phytic acid (~5 mM), 200 mM sodium acetate, pH 5.0. After 15 min incubation at 37°C, the reaction was stopped by addition of an equal volume of 15% trichloroacetic acid. The liberated phosphate ions were quantified by mixing 100 µl of the assay mixture with 900 µl H<sub>2</sub>O and 1 ml of 0.6 M H<sub>2</sub>SO<sub>4</sub>, 2% ascorbic acid and 0.5% ammonium molybdate. Standard solutions of potassium phosphate were used as reference.

[0058] In case of pH optimum curves, purified enzymes were diluted in 10 mM sodium acetate, pH 5.0. Incubations were started by mixing aliquots of the diluted protein with an equal volume of 1% phytic acid (~10 mM) in a series of different buffers: 0.4 M glycine/HCl, pH 2.5; 0.4 M acetate/NaOH, pH 3.0, 3.5, 4.0, 4.5, 5.0, 5.5; 0.4 M imidazole/HCl, pH 6.0, 6.5; 0.4 M Tris/HCl, pH 7.0, 7.5, 8.0, 8.5, 9.0. Control experiments showed that pH was only slightly affected by the mixing step. Incubations were performed for 15 min at 37°C as described above.

[0059] For determination of the substrate specificities of wild-type and mutant *A. fumigatus* phytases, phytic acid in the assay mixture was replaced by 5 mM-concentrations of the respective phosphate compounds. The activity tests were performed as described above.

[0060] Protein concentrations were calculated from the OD at 280 nm, using theoretical absorption values calculated from the known protein sequences with the DNA\* software (DNASTAR, Inc., Madison, Wisconsin, USA). An absorption of 1.0 OD at 280 nm corresponds to 0.94 mg/ml *A. fumigatus* phytase and 0.85 mg/ml of *A. terreus* CBS116.46 phytase.

[0061] pH profiles of *Aspergillus fumigatus* mutants T1 (Q27L), T5 (Q27L, Q274L) and T6 (Q27L, Q274L, G277D) have drastically changed compared to the wild-type *A. fumigatus* phytase (see Figure 2). All mutants showed equal pH profiles. Increase in specific activity at pH 5.0 of the mureins as compared to the wild-type phytase of *Aspergillus fumigatus* is shown in Table 2. Enzyme activities were measured under standard assay conditions at pH 5.0. Several individual measurements (n: number of assays) were averaged.

[0062] The pH profile of *A. fumigatus* phytase mutant Q27A resembles the pH profile of *A. fumigatus* wild-type phytase over nearly the whole pH range (Figure 20). Whereas the specific activity of wild-type phytase is decreasing at pH values below pH 4.0, the specific activity of the phytase mutant Q27A remains nearly constant down to pH 2.9.

[0063] The single amino acid exchanges Q27L, Q27I, Q27V or Q27T have remarkably increased the specific activity over the whole pH range, especially between pH 5.0 and 7.5 (Figure 20). Maximum values are reached at pH 6.5. In addition, mutation Q27T caused the highest specific activity values for phytic acid at low pH (pH 3.0-5.0).

[0064] Higher specific activities are also gained by the single mutations Q27G or Q27N, between pH 2.5 and 7.0, with maximum values at pH 6.0 (Figure 20). The specific activity decreases at pH values below 3.5.

[0065] All single mutants still show a broad substrate specificity which is comparable to that of *A. fumigatus* wild-type phytase (Figure 21). Some of the mutants show significantly higher specific activities than other mutants for selected

substrates, e. g., the Q27T mutant for p-nitrophenyl phosphate and ATP, or the Q27G mutant for phosphoenolpyruvate.

[0066] As shown in Figure 22 the combination of mutation Q27L with S66D or S140Y and D141G led to a shift of the pH profile towards lower pH. The maximum specific activity gained by the single mutation Q27L is further increased by the additional amino acid exchanges.

5 [0067] As shown in Figure 3, *Aspergillus fumigatus* phytase mutant T1 (Q27L) showed no difference in substrate specificity compared to the triple mutant T6 (Q27L, Q274L, G277D).

[0068] The pH profiles of the mutoins N1-6, except N2 show significant differences compared to the wild-type phytase (Fig. 10). Whereas the pH profile of mutoin N4 is expanded towards lower pH, the profiles of mutoins N3 to N6 are shifted towards lower pH. The mutoins N5, N6 reach maximum activity already at pH 3.0.

10 [0069] The mutoins N1 to N6 show in almost all cases a drastic reduction in specific activity for all tested substrates, except for phytic acid (Fig. 9). Specific activity for phytic acid remained unchanged compared to the wild-type phytase, whereas mutant N3 and N6 show a tendential higher activity (Fig. 19).

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**Table 1****A) Mutations towards *A. terreus* cbs116.46 phytase**

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Mutation	T1	T2	T3	T4	T5	T6	T7
Q27L	X				X	X	X
Q274L		X			X	X	X
G277D			X			X	X
N340S				X			X

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**B) Mutations towards *A. niger* (*ficum*) phytase**

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Mutation	N1	N2	N3	N4	N5	N6
G277K	X			X	X	X
A205E		X		X		X
Y282H			X		X	X

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**Table 2**

		U/mg
<i>A. fumigatus</i> wild-type phytase	26.5 ± 5.2	22

Table 2 (continued)

		U/mg
5	<i>A. fumigatus</i> Q27L	83.4
	<i>A. fumigatus</i> Q27L, Q274L	88.7 ± 13.5
	<i>A. fumigatus</i> Q27L, Q274L, G277D	92.3 + 12.0
	<i>A. terreus</i> cbs116.46 phytase	195.8±17.8
10		7

Table 3

Specific activity under standard assay conditions at pH 5.0. Average standard deviation is 10%.		
	Specific activity [U/mg]	Number of independent assays
15	<i>A. fumigatus</i> wild-type phytase	26.5
20	<i>A. fumigatus</i> Q27N	45.5
25	<i>A. fumigatus</i> Q27T	106.9
	<i>A. fumigatus</i> Q27L	83.4
	<i>A. fumigatus</i> Q27I	91.2
	<i>A. fumigatus</i> Q27V	35.0
	<i>A. fumigatus</i> Q27A	27.3
30	<i>A. fumigatus</i> Q27G	59.6
	<i>A. fumigatus</i> Q27L-S66D	118.5
	<i>A. fumigatus</i> Q27L-S140Y-D141G	193.0

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Example 8

[0070] As an alternative approach to obtain phytases with modified characteristics and to get a better idea about the natural variation found in phytase characteristics within a certain species, naturally occurring variants of *A. fumigatus* phytase were analysed. Phytase genes were obtained from six different isolates of *A. fumigatus*. The amino acid sequence of phytase from two of the *A. fumigatus* isolates (ATCC 26934 and ATCC 34625) showed no difference to the original amino acid sequence of wild-type *A. fumigatus* phytase ATCC 13073. Phytase from three other isolates had one or two amino acid substitutions, none of which directly affected the active site. Enzymatic characteristics remained unaffected by these substitutions (not shown). The phytase of isolate of *A. fumigatus* (ATCC 32239) differed in 13 positions in the signal sequence and 51 positions in the mature part of the protein compared to the original wild-type *A. fumigatus* phytase (ATCC 13073). Several of these substitutions affect variable amino acids of the active site cavity. This resulted in an increase in specific activity with phytic acid as substrate (47 U/mg, standard enzyme assay) and in loss of enzymatic activity above pH 7 (Fig. 24). Also in this case, the specific activity against phytic acid was increased relative to the specific activities with other substrates (Fig. 25).

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Example 9

[0071] Construction of plasmids pc-S130N, pc-R129L-S130N, pc-K167G-R168Q encoding *A. fumigatus* [ATCC 13073] phytase S130N single mutant and R129L-S130N double mutant and *A. nidulans* phytase K167G-R168Q double mutant was basically carried out as described in Example 3. Plasmid pUC18-AfumcDNA was used as template for site directed mutagenesis together with the corresponding primer sets L, M and N (Figure 14a; Figure 26).

[0072] All mutations were verified by DNA sequence analysis of the entire gene.

Example 10

- [0073] When expressed in *A. niger* and stored as concentrated culture supernatants at 4°C, the phytases from *A. fumigatus*, *A. nidulans* displayed tendency to undergo proteolytic degradation. N-terminal sequencing of fragments suggested that cleavage occurred between amino acids S130-V131 and K167-R168 or R168-A169, respectively. Compared with 3D structure of *A. niger* phytase revealed that all cleavage sites are found within surface-exposed loop structures and are therefore accessible to proteases.
- [0074] Site-directed mutagenesis at protease-sensitive sites of *A. fumigatus* phytase (S130N, R129L-S130N) and *A. nidulans* phytase (K167G-R168Q) yielded mutant proteins with considerably reduced susceptibility to proteolysis.
- [0075] In contrast to expression in *A. niger*, proteolytic degradation was not observed when the phytases were expressed in *Hansenula polymorpha*.

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## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

5

## (i) APPLICANT:

- (A) NAME: F. Hoffmann-La Roche AG
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10

(ii) TITLE OF INVENTION: Modified Phytases

15

(iii) NUMBER OF SEQUENCES: 8

## (iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

20

## (v) CURRENT APPLICATION DATA:

APPLICATION NUMBER: EP 98104858.0

## (2) INFORMATION FOR SEQ ID NO: 1:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1931 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: DNA (genomic)

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION:join(158..204, 259..1600)

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TCTGTAAACCG ATAGCGGACC GACTAGGCAT CGTTGATCCA CAATATCTCA GACAATGC<sup>60</sup>AA

40

CTCAGTCGAA TATGAAGGGC TACAGCCAGC ATTTAAATAC GGCCGTCTAG GTGGGGCTCC<sup>120</sup>GGGGATGAGG AGGAGCAGGC TCGTGTTCAT TTCGGTC ATG GCT TTT TTC ACG GTC<sup>175</sup>Met Ala Phe Phe Thr Val  
1 5

45

GCT CTT TCG CTT TAT TAC TTG CTA TCG AG GTGAGATCTC TACAATATCT

224

Ala Leu Ser Leu Tyr Tyr Leu Leu Ser Arg  
10 15

50

GTCTGCTTAG TTGAATTGGT ACTTATCTGT ACAG A GTC TCT GCT CAG GCC CCA<sup>277</sup>Val Ser Ala Gln Ala Pro  
20

55

GTG GTC CAG AAT CAT TCA TGC AAT ACG GCG GAC GGT GGA TAT CAA TGC  
 325  
 Val Val Gln Asn His Ser Cys Asn Thr Ala Asp Gly Gly Tyr Gln Cys  
 25 30 35  
 5  
 TTC CCC AAT GTC TCT CAT GTT TGG GGT CAG TAC TCG CCG TAC TTC TCC  
 373  
 Phe Pro Asn Val Ser His Val Trp Gly Gln Tyr Ser Pro Tyr Phe Ser  
 40 45 50  
 10 ATC GAG CAG GAG TCA GCT ATC TCT GAG GAC GTG CCT CAT GGC TGT GAG  
 421  
 Ile Glu Gln Glu Ser Ala Ile Ser Glu Asp Val Pro His Gly Cys Glu  
 55 60 65 70  
 15 GTT ACC TTT GTG CAG GTG CTC TCG CGG CAT GGG GCT AGG TAT CCG ACA  
 469  
 Val Thr Phe Val Gln Val Leu Ser Arg His Gly Ala Arg Tyr Pro Thr  
 75 80 85  
 20 GAG TCG AAG AGT AAG GCG TAC TCG GGG TTG ATT GAA GCA ATC CAG AAG  
 517  
 Glu Ser Lys Ser Lys Ala Tyr Ser Gly Leu Ile Glu Ala Ile Gln Lys  
 90 95 100  
 25 AAT GCT ACC TCT TTT TGG GGA CAG TAT GCT TTT CTG GAG AGT TAT AAC  
 565  
 Asn Ala Thr Ser Phe Trp Gly Gln Tyr Ala Phe Leu Glu Ser Tyr Asn  
 105 110 115  
 30 TAT ACC CTC GGC GCG GAT GAC TTG ACT ATC TTC GGC GAG AAC CAG ATG  
 613  
 Tyr Thr Leu Gly Ala Asp Asp Leu Thr Ile Phe Gly Glu Asn Gln Met  
 120 125 130  
 GTT GAT TCG GGT GCC AAG TTC TAC CGA CGG TAT AAG AAT CTC GCC AGG  
 661  
 Val Asp Ser Gly Ala Lys Phe Tyr Arg Arg Tyr Lys Asn Leu Ala Arg  
 135 140 145 150  
 35 AAA AAT ACT CCT TTT ATC CGT GCA TCA GGG TCT GAC CGT GTC GTT GCG  
 709  
 Lys Asn Thr Pro Phe Ile Arg Ala Ser Gly Ser Asp Arg Val Val Ala  
 155 160 165  
 40 TCT GCG GAG AAG TTC ATT AAT GGA TTT CGC AAG GCT CAG CTC CAC GAC  
 757  
 Ser Ala Glu Lys Phe Ile Asn Gly Phe Arg Lys Ala Gln Leu His Asp  
 170 175 180  
 CAT GGC TCC AAA CGT GCT ACG CCA GTT GTC AAT GTG ATT ATC CCT GAA  
 805  
 His Gly Ser Lys Arg Ala Thr Pro Val Val Asn Val Ile Ile Pro Glu  
 185 190 195  
 45 ATC GAT GGG TTT AAC AAC ACC CTG GAC CAT AGC ACG TGC GTA TCT TTT  
 853  
 Ile Asp Gly Phe Asn Asn Thr Leu Asp His Ser Thr Cys Val Ser Phe  
 200 205 210  
 GAG AAT GAT GAG CGG GCG GAT GAA ATT GAA GCC AAT TTC ACG GCA ATT  
 901  
 Glu Asn Asp Glu Arg Ala Asp Glu Ile Glu Ala Asn Phe Thr Ala Ile  
 215 220 225 230  
 50 ATG GGA CCT CCG ATC CGC AAA CGT CTG GAA AAT GAC CTC CCT GGC ATC  
 949  
 Met Gly Pro Pro Ile Arg Lys Arg Leu Glu Asn Asp Leu Pro Gly Ile  
 235 240 245

AAA CTT ACA AAC GAG AAT GTA ATA TAT TTG ATG GAT ATG TGC TCT TTC  
 997  
 Lys Leu Thr Asn Glu Asn Val Ile Tyr Leu Met Asp Met Cys Ser Phe  
 250 255 260  
 5

GAC ACC ATG GCG CGC ACC GCC CAC GGA ACC GAG CTG TCT CCA TTT TGT  
 1045  
 Asp Thr Met Ala Arg Thr Ala His Gly Thr Glu Leu Ser Pro Phe Cys  
 265 270 275

10

GCC ATC TTC ACT GAA AAG GAG TGG CTG CAG TAC GAC TAC CTT CAA TCT  
 1093  
 Ala Ile Phe Thr Glu Lys Glu Trp Leu Gln Tyr Asp Tyr Leu Gln Ser  
 280 285 290

15

CTA TCA AAG TAC TAC GGC TAC GGT GCC GGA AGC CCC CTT GGC CCA GCT  
 1141  
 Leu Ser Lys Tyr Tyr Gly Ala Gly Ser Pro Leu Gly Pro Ala  
 295 300 305 310

CAG GGA ATT GGC TTC ACC AAC GAG CTG ATT GCC CGA CTA ACG CAA TCG  
 1189  
 Gln Gly Ile Gly Phe Thr Asn Glu Leu Ile Ala Arg Leu Thr Gln Ser  
 315 320 325

20

CCC GTC CAG GAC AAC ACA AGC ACC AAC CAC ACT CTA GAC TCG AAC CCA  
 1237  
 Pro Val Gln Asp Asn Thr Ser Thr Asn His Thr Leu Asp Ser Asn Pro  
 330 335 340

25

GCC ACA TTT CCG CTC GAC AGG AAG CTC TAC GCC GAC TTC TCC CAC GAC  
 1285  
 Ala Thr Phe Pro Leu Asp Arg Lys Leu Tyr Ala Asp Phe Ser His Asp  
 345 350 355

AAT AGC ATG ATA TCG ATA TTC TTC GCC ATG GGT CTG TAC AAC GGC ACC  
 1333  
 Asn Ser Met Ile Ser Ile Phe Phe Ala Met Gly Leu Tyr Asn Gly Thr  
 360 365 370

CAG CCG CTG TCA ATG GAT TCC GTG GAG TCG ATC CAG GAG ATG GAC GGT  
 1381  
 Gln Pro Leu Ser Met Asp Ser Val Glu Ser Ile Gln Glu Met Asp Gly  
 375 380 385 390

35

TAC GCG GCG TCT TGG ACT GTT CCG TTT GGT GCG AGG GCT TAC TTT GAG  
 1429  
 Tyr Ala Ala Ser Trp Thr Val Pro Phe Gly Ala Arg Ala Tyr Phe Glu  
 395 400 405

40

CTC ATG CAG TGC GAG AAG GAG CCG CTT GTG CGG GTA TTA GTG AAT  
 1477  
 Leu Met Gln Cys Glu Lys Lys Glu Pro Leu Val Arg Val Leu Val Asn  
 410 415 420

GAT CGC GTT GTT CCT CTT CAT GGC TGC GCA GTT GAC AAG TTT GGA CGG  
 1525  
 Asp Arg Val Val Pro Leu His Gly Cys Ala Val Asp Lys Phe Gly Arg  
 425 430 435

45

TGC ACT TTG GAC GAT TGG GTA GAG GGC TTG AAT TTT GCA AGG AGC GGC  
 1573  
 Cys Thr Leu Asp Asp Trp Val Glu Gly Leu Asn Phe Ala Arg Ser Gly  
 440 445 450

50

GGG AAC TGG AAG ACT TGT TTT ACC CTA TAAAGGGCGT TTGCTCATTC  
 1620  
 Gly Asn Trp Lys Thr Cys Phe Thr Leu  
 455 460

ATAAGTGGTG TGCAGGTATA GGAAGGTTAG GGAATTAGCT GTTTGGCTTT ACTCTTATTA  
 1680

5 GACCAAGAAT GATTGTTTG TTCTCAAGGC CTTCTAGCAT ATCGTCAAGT GGGATAAAC  
 1740

ACCTATCCTC CATGTGTTAGG TGAACCCGCT CTTGCATCAA CCTCTTGTGT TTCAGAGTAG  
 1800

10 TTTCACCAAA CATATCCTCG TGTCCCTCTCT TCTGCTCTTC GGTCTCATAT TACACTGTT  
 1860

TCTATCTATA TCGTCAACAA AACTACCACC CAAACACCAA ATGTCACACT TTCCAGCACG  
 1920

15 AAATTTCTTC G  
 1931

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 463 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

	Met Ala Phe Phe Thr Val Ala Leu Ser Leu Tyr Tyr Leu Leu Ser Arg
	1 5 10 15
25	Val Ser Ala Gln Ala Pro Val Val Gln Asn His Ser Cys Asn Thr Ala
	20 25 30
	Asp Gly Gly Tyr Gln Cys Phe Pro Asn Val Ser His Val Trp Gly Gln
	35 40 45
30	Tyr Ser Pro Tyr Phe Ser Ile Glu Gln Glu Ser Ala Ile Ser Glu Asp
	50 55 60
	Val Pro His Gly Cys Glu Val Thr Phe Val Gln Val Leu Ser Arg His
	65 70 75 80
35	Gly Ala Arg Tyr Pro Thr Glu Ser Lys Ser Lys Ala Tyr Ser Gly Leu
	85 90 95
	Ile Glu Ala Ile Gln Lys Asn Ala Thr Ser Phe Trp Gly Gln Tyr Ala
	100 105 110
	Phe Leu Glu Ser Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu Thr Ile
	115 120 125
40	Phe Gly Glu Asn Gln Met Val Asp Ser Gly Ala Lys Phe Tyr Arg Arg
	130 135 140
	Tyr Lys Asn Leu Ala Arg Lys Asn Thr Pro Phe Ile Arg Ala Ser Gly
	145 150 155 160
45	Ser Asp Arg Val Val Ala Ser Ala Glu Lys Phe Ile Asn Gly Phe Arg
	165 170 175
	Lys Ala Gln Leu His Asp His Gly Ser Lys Arg Ala Thr Pro Val Val
	180 185 190
50	Asn Val Ile Ile Pro Glu Ile Asp Gly Phe Asn Asn Thr Leu Asp His
	195 200 205
	Ser Thr Cys Val Ser Phe Glu Asn Asp Glu Arg Ala Asp Glu Ile Glu
	210 215 220

Ala Asn Phe Thr Ala Ile Met Gly Pro Pro Ile Arg Lys Arg Leu Glu  
 225 230 235 240  
 5 Asn Asp Leu Pro Gly Ile Lys Leu Thr Asn Glu Asn Val Ile Tyr Leu  
 245 250 255  
 Met Asp Met Cys Ser Phe Asp Thr Met Ala Arg Thr Ala His Gly Thr  
 260 265 270  
 10 Glu Leu Ser Pro Phe Cys Ala Ile Phe Thr Glu Lys Glu Trp Leu Gln  
 275 280 285  
 Tyr Asp Tyr Leu Gln Ser Leu Ser Lys Tyr Tyr Gly Tyr Gly Ala Gly  
 290 295 300  
 15 Ser Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr Asn Glu Leu Ile  
 305 310 315 320  
 Ala Arg Leu Thr Gln Ser Pro Val Gln Asp Asn Thr Ser Thr Asn His  
 325 330 335  
 Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asp Arg Lys Leu Tyr  
 340 345 350  
 20 Ala Asp Phe Ser His Asp Asn Ser Met Ile Ser Ile Phe Phe Ala Met  
 355 360 365  
 Gly Leu Tyr Asn Gly Thr Gln Pro Leu Ser Met Asp Ser Val Glu Ser  
 370 375 380  
 25 Ile Gln Glu Met Asp Gly Tyr Ala Ala Ser Trp Thr Val Pro Phe Gly  
 385 390 395 400  
 Ala Arg Ala Tyr Phe Glu Leu Met Gln Cys Glu Lys Lys Glu Pro Leu  
 405 410 415  
 Val Arg Val Leu Val Asn Asp Arg Val Val Pro Leu His Gly Cys Ala  
 30 420 425 430  
 Val Asp Lys Phe Gly Arg Cys Thr Leu Asp Asp Trp Val Glu Gly Leu  
 435 440 445  
 Asn Phe Ala Arg Ser Gly Gly Asn Trp Lys Thr Cys Phe Thr Leu  
 450 455 460  
 35 (2) INFORMATION FOR SEQ ID NO: 3:  
 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1845 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 40 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: DNA (genomic)  
 (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 45 (B) LOCATION:join(288..334, 390..1740)  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 TTCCACGCTG AAAGCCTGAC TCGGATTTC CAGGCTGCTC AACTGCCTGC  
 50 60  
 TTATCTTCAT CAGACGCAGA TACACAACCT GGTCTGTAGA TGCACCCATG ACGGACGAAC  
 120

GCACCGCTCT CTTGGCCTCC AGGGACCCGG AGGTCGAGGG CGATGAGGTC GCGCCCTCGA  
 180

5 CGGCCTCCC GTCCCTGTTG CAGTTGAGAT CTCGCTGCGA ACGTCGACCG CAGATATGGT  
 240

TGTCTTCGAC GTTTCTCGC CTTCGAGGAA GAATTGCTGC TGTGACG ATG AGT CTG  
 296

Met Ser Leu  
1

10 TTG TTG CTG GTG CTG TCC GGC GGG TTG GTC GCG TTA TA GTATGCTCCT  
 344  
 Leu Leu Leu Val Leu Ser Gly Gly Leu Val Ala Leu Tyr  
 5 10 15

15 TCTCTCTGGT CATATTGTTT TCTGCTAACG TTCTCATAAT TGAAG T GTC TCA AGA  
 399

Val Ser Arg

20 AAT CCG CAT GTT GAT AGC CAC TCT TGC AAT ACA GTG GAA GGA GGG TAT  
 447  
 Asn Pro His Val Asp Ser His Ser Cys Asn Thr Val Glu Gly Gly Tyr  
 20 25 30 35

25 CAG TGT CGT CCA GAA ATC TCC CAC TCC TGG GGC CAG TAT TCT CCA TTC  
 495  
 Gln Cys Arg Pro Glu Ile Ser His Ser Trp Gly Gln Tyr Ser Pro Phe  
 40 45 50

30 TTC TCC CTG GCA GAC CAG TCG GAG ATC TCG CCA GAT GTC CCA CAG AAC  
 543  
 Phe Ser Leu Ala Asp Gln Ser Glu Ile Ser Pro Asp Val Pro Gln Asn  
 55 60 65

35 TGC AAG ATT ACG TTT GTC CAG CTG CTT TCT CGT CAC GGC GCT AGA TAC  
 591  
 Cys Lys Ile Thr Phe Val Gln Leu Leu Ser Arg His Gly Ala Arg Tyr  
 70 75 80

40 CCT ACG TCT TCC AAG ACG GAG CTG TAT TCG CAG CTG ATC AGT CGG ATT  
 639  
 Pro Thr Ser Ser Lys Thr Glu Leu Tyr Ser Gln Leu Ile Ser Arg Ile  
 85 90 95

45 CAG AAG ACG GCG ACT GCG TAC AAA GGC TAC TAT GCC TTC TTG AAA GAC  
 687  
 Gln Lys Thr Ala Thr Ala Tyr Lys Gly Tyr Tyr Ala Phe Leu Lys Asp  
 100 105 110 115

50 TAC AGA TAC CAG CTG GGA GCG AAC GAC CTG ACG CCC TTT GGG GAA AAC  
 735  
 Tyr Arg Tyr Gln Leu Gly Ala Asn Asp Leu Thr Pro Phe Gly Glu Asn  
 120 125 130

55 CAG ATG ATC CAG TTG GGC ATC AAG TTT TAT AAC CAT TAC AAG AGT CTC  
 783  
 Gln Met Ile Gln Leu Gly Ile Lys Phe Tyr Asn His Tyr Lys Ser Leu  
 135 140 145

60 GCC AGG AAT GCC GTC CCA TTC GTT CGT TGC TCC GGC TCT GAT CGG GTC  
 831  
 Ala Arg Asn Ala Val Pro Phe Val Arg Cys Ser Gly Ser Asp Arg Val  
 150 155 160

65 ATT GCC TCG GGG AGA CTT TTC ATC GAA GGT TTC CAG AGC GCC AAA GTG  
 879  
 Ile Ala Ser Gly Arg Leu Phe Ile Glu Gly Phe Gln Ser Ala Lys Val  
 165 170 175

CTG GAT CCT CAT TCA GAC AAG CAT GAC GCT CCT CCC ACG ATC AAC GTG  
 927  
 Leu Asp Pro His Ser Asp Lys His Asp Ala Pro Pro Thr Ile Asn Val  
 180 185 190 195  
 5  
 ATC ATC GAG GAG GGT CCG TCC TAC AAT AAC ACG CTC GAC ACC GGC AGC  
 975  
 Ile Ile Glu Glu Gly Pro Ser Tyr Asn Asn Thr Leu Asp Thr Gly Ser  
 200 205 210  
 10  
 TGT CCA GTC TTT GAG GAC AGC AGC GGG GGA CAT GAC GCA CAG GAA AAG  
 1023  
 Cys Pro Val Phe Glu Asp Ser Ser Gly Gly His Asp Ala Gln Glu Lys  
 215 220 225  
 15  
 TTC GCA AAG CAA TTC GCA CCA GCT ATC CTG GAA AAG ATC AAG GAC CAT  
 1071  
 Phe Ala Lys Gln Phe Ala Pro Ala Ile Leu Glu Lys Ile Lys Asp His  
 230 235 240  
 20  
 CTT CCC GGC GTG GAC CTG GCC GTG TCG GAT GTA CCG TAC TTG ATG GAC  
 1119  
 Leu Pro Gly Val Asp Leu Ala Val Ser Asp Val Pro Tyr Leu Met Asp  
 245 250 255  
 TTG TGT CCG TTT GAG ACC TTG GCT CGC AAC CAC ACA GAC ACG CTG TCT  
 1167  
 Leu Cys Pro Phe Glu Thr Leu Ala Arg Asn His Thr Asp Thr Leu Ser  
 260 265 270 275  
 25  
 CCG TTC TGC GCT CTT TCC ACG CAA GAG GAG TGG CAA GCA TAT GAC TAC  
 1215  
 Pro Phe Cys Ala Leu Ser Thr Gln Glu Glu Trp Gln Ala Tyr Asp Tyr  
 280 285 290  
 30  
 TAC CAA AGT CTG GGG AAA TAC TAT GGC AAT GGC GGG GGT AAC CCG TTG  
 1263  
 Tyr Gln Ser Leu Gly Lys Tyr Tyr Gly Asn Gly Gly Asn Pro Leu  
 295 300 305  
 GGG CCA GCC CAA GGC GTG GGG TTT GTC AAC GAG TTG ATT GCT CGC ATG  
 1311  
 Gly Pro Ala Gln Gly Val Gly Phe Val Asn Glu Leu Ile Ala Arg Met  
 310 315 320  
 35  
 ACC CAT AGC CCT GTC CAG GAC TAC ACC ACG GTC AAC CAC ACT CTT GAC  
 1359  
 Thr His Ser Pro Val Gln Asp Tyr Thr Thr Val Asn His Thr Leu Asp  
 325 330 335  
 TCG AAT CCG GCG ACA TTC CCT TTG AAC GCG ACG CTG TAC GCA GAT TTC  
 1407  
 Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe  
 340 345 350 355  
 40  
 AGC CAC GAC AAC ACA ATG ACG TCA ATT TTC GCG GCC TTG GGC CTG TAC  
 1455  
 Ser His Asp Asn Thr Met Thr Ser Ile Phe Ala Ala Leu Gly Leu Tyr  
 360 365 370  
 45  
 AAC GGG ACC GCG AAG CTG TCC ACG ACC GAG ATC AAG TCC ATT GAA GAG  
 1503  
 Asn Gly Thr Ala Lys Leu Ser Thr Thr Glu Ile Lys Ser Ile Glu Glu  
 375 380 385  
 50  
 ACG GAC GGC TAC TCG GCG GCG TGG ACC GTT CCG TTC GGG GGG CGA GCC  
 1551  
 Thr Asp Gly Tyr Ser Ala Ala Trp Thr Val Pro Phe Gly Gly Arg Ala  
 390 395 400

TAT ATC GAG ATG ATG CAG TGT GAT GAT TCG GAT GAG CCA GTC GTT CGG  
 1599  
 Tyr Ile Glu Met Met Gln Cys Asp Asp Ser Asp Glu Pro Val Val Arg  
 405 410 415  
 5  
 GTG CTG GTC AAC GAC CGG GTG GTG CCA CTG CAT GGC TGC GAG GTG GAC  
 1647  
 Val Leu Val Asn Asp Arg Val Val Pro Leu His Gly Cys Glu Val Asp  
 420 425 430 435  
 10  
 TCC CTG GGG CGA TGC AAA CGA GAC GAC TTT GTC AGG GGA CTG AGT TTT  
 1695  
 Ser Leu Gly Arg Cys Lys Arg Asp Asp Phe Val Arg Gly Leu Ser Phe  
 440 445 450  
 15  
 GCG CGA CAG GGT GGG AAC TGG GAG GGG TGT TAC GCT GCT TCT GAG  
 1740  
 Ala Arg Gln Gly Gly Asn Trp Glu Gly Cys Tyr Ala Ala Ser Glu  
 455 460 465  
 TAGGTTTATT CAGCGAGTTT CGACCTTCT ATCCTTCAAA CACTGCACAA AGACACACTG  
 1800  
 20  
 CATGAAATGG TAACAGGCCT GGAGCGTTT AGAAGGAAAA AAGTT  
 1845

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 466 amino acids  
 25 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Met Ser Leu Leu Leu Leu Val Leu Ser Gly Gly Leu Val Ala Leu Tyr  
 1 5 10 15  
 30 Val Ser Arg Asn Pro His Val Asp Ser His Ser Cys Asn Thr Val Glu  
 20 25 30  
 Gly Gly Tyr Gln Cys Arg Pro Glu Ile Ser His Ser Trp Gly Gln Tyr  
 35 40 45  
 35 Ser Pro Phe Phe Ser Leu Ala Asp Gln Ser Glu Ile Ser Pro Asp Val  
 50 55 60  
 Pro Gln Asn Cys Lys Ile Thr Phe Val Gln Leu Leu Ser Arg His Gly  
 65 70 75 80  
 40 Ala Arg Tyr Pro Thr Ser Ser Lys Thr Glu Leu Tyr Ser Gln Leu Ile  
 85 90 95  
 Ser Arg Ile Gln Lys Thr Ala Thr Ala Tyr Lys Gly Tyr Tyr Ala Phe  
 100 105 110  
 45 Leu Lys Asp Tyr Arg Tyr Gln Leu Gly Ala Asn Asp Leu Thr Pro Phe  
 115 120 125  
 Gly Glu Asn Gln Met Ile Gln Leu Gly Ile Lys Phe Tyr Asn His Tyr  
 130 135 140  
 50 Lys Ser Leu Ala Arg Asn Ala Val Pro Phe Val Arg Cys Ser Gly Ser  
 145 150 155 160  
 Asp Arg Val Ile Ala Ser Gly Arg Leu Phe Ile Glu Gly Phe Gln Ser  
 165 170 175

55

Ala Lys Val Leu Asp Pro His Ser Asp Lys His Asp Ala Pro Pro Thr  
 180 185 190  
 Ile Asn Val Ile Ile Glu Glu Gly Pro Ser Tyr Asn Asn Thr Leu Asp  
 5 195 200 205  
 Thr Gly Ser Cys Pro Val Phe Glu Asp Ser Ser Gly Gly His Asp Ala  
 210 215 220  
 Gln Glu Lys Phe Ala Lys Gln Phe Ala Pro Ala Ile Leu Glu Lys Ile  
 10 225 230 235 240  
 Lys Asp His Leu Pro Gly Val Asp Leu Ala Val Ser Asp Val Pro Tyr  
 245 250 255  
 Leu Met Asp Leu Cys Pro Phe Glu Thr Leu Ala Arg Asn His Thr Asp  
 260 265 270  
 Thr Leu Ser Pro Phe Cys Ala Leu Ser Thr Gln Glu Glu Trp Gln Ala  
 15 275 280 285  
 Tyr Asp Tyr Tyr Gln Ser Leu Gly Lys Tyr Tyr Gly Asn Gly Gly  
 290 295 300  
 Asn Pro Leu Gly Pro Ala Gln Gly Val Gly Phe Val Asn Glu Leu Ile  
 20 305 310 315 320  
 Ala Arg Met Thr His Ser Pro Val Gln Asp Tyr Thr Thr Val Asn His  
 325 330 335  
 Thr Leu Asp Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr Leu Tyr  
 25 340 345 350  
 Ala Asp Phe Ser His Asp Asn Thr Met Thr Ser Ile Phe Ala Ala Leu  
 355 360 365  
 Gly Leu Tyr Asn Gly Thr Ala Lys Leu Ser Thr Thr Glu Ile Lys Ser  
 30 370 375 380  
 Ile Glu Glu Thr Asp Gly Tyr Ser Ala Ala Trp Thr Val Pro Phe Gly  
 385 390 395 400  
 Gly Arg Ala Tyr Ile Glu Met Met Gln Cys Asp Asp Ser Asp Glu Pro  
 405 410 415  
 Val Val Arg Val Leu Val Asn Asp Arg Val Val Pro Leu His Gly Cys  
 45 420 425 430  
 Glu Val Asp Ser Leu Gly Arg Cys Lys Arg Asp Asp Phe Val Arg Gly  
 435 440 445  
 Leu Ser Phe Ala Arg Gln Gly Asn Trp Glu Gly Cys Tyr Ala Ala  
 40 450 455 460  
 Ser Glu  
 465

## (2) INFORMATION FOR SEQ ID NO: 5:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1571 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

55

(A) NAME/KEY: CDS  
 (B) LOCATION:join(43..89, 147..1494)

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

AGATTCAACG ACGGAGGAAT CGCAACCCTA ATTGTGGTA TC ATG GTG ACT CTG

54

Met Val Thr Leu  
1

10

ACT TTC CTG CTT TCG GCG GCG TAT CTG CTT TCT GG GTGAGTGGCT

99

Thr Phe Leu Leu Ser Ala Ala Tyr Leu Leu Ser Gly  
5 10 15

15

TGGATCTATT GCTCGGATAG GGCTGTGGTG CTGATTCTGA AACGGAG T AGA GTG  
153

Arg Val

20

TCT GCG GCA CCT AGT TCT GCT GGC TCC AAG TCC TGC GAT ACG GTA GAC  
201  
Ser Ala Ala Pro Ser Ser Ala Gly Ser Lys Ser Cys Asp Thr Val Asp  
20 25 30

25

CTC GGG TAC CAG TGC TCC CCT GCG ACT TCT CAT CTA TGG GGC CAG TAC  
249  
Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu Trp Gly Gln Tyr  
35 40 45 50

30

TCG CCA TTC TTT TCG CTC GAG GAC GAG CTG TCC GTG TCG AGT AAG CTT  
297  
Ser Pro Phe Phe Ser Leu Glu Asp Glu Leu Ser Val Ser Ser Lys Leu  
55 60 65

35

CCC AAG GAT TGC CGG ATC ACC TTG GTA CAG GTG CTA TCG CGC CAT GGA  
345  
Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu Ser Arg His Gly  
70 75 80GCG CGG TAC CCA ACC AGC TCC AAG AGC AAA AAG TAT AAG AAG CTT GTG  
393  
Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Lys Tyr Lys Lys Leu Val  
85 90 95

40

ACG GCG ATC CAG GCC AAT GCC ACC GAC TTC AAG GGC AAG TTT GCC TTT  
441  
Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly Lys Phe Ala Phe  
100 105 110

45

TTG AAG ACG TAC AAC TAT ACT CTG GGT GCG GAT GAC CTC ACT CCC TTT  
489  
Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu Thr Pro Phe  
115 120 125 130

50

GGG GAG CAG CAG CTG GTG AAC TCG GGC ATC AAG TTC TAC CAG AGG TAC  
537  
Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln Arg Tyr  
135 140 145

55

AAG GCT CTG GCG CGC AGT GTG GTG CCG TTT ATT CGC GCC TCA GGC TCG  
585  
Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg Ala Ser Gly Ser  
150 155 160GAC CGG GTT ATT GCT TCG GGA GAG AAG TTC ATC GAG GGG TTC CAG CAG  
633  
Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu Gly Phe Gln Gln  
165 170 175

GCG AAG CTG GCT GAT CCT GGC GCG ACG AAC CGC GCC GCT CCG GCG ATT  
 681  
 Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala Ala Pro Ala Ile  
 180 185 190  
 5  
 AGT GTG ATT ATT CCG GAG AGC GAG TTC AAC AAT ACG CTG GAC CAC  
 729  
 Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn Thr Leu Asp His  
 195 200 205 210  
 10  
 GGT GTG TGC ACG AAG TTT GAG GCG AGT CAG CTG GGA GAT GAG GTT GCG  
 777  
 Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly Asp Glu Val Ala  
 215 220 225  
 15  
 GCC AAT TTC ACT GCG CTC TTT GCA CCC GAC ATC CGA GCT CGC GCC GAG  
 825  
 Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg Ala Arg Ala Glu  
 230 235 240  
 AAG CAT CTT CCT GGC GTG ACG CTG ACA GAC GAG GAC GTT GTC AGT CTA  
 873  
 Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp Val Val Ser Leu  
 245 250 255  
 20  
 ATG GAC ATG TGT TCG TTT GAT ACG GTA GCG CGC ACC AGC GAC GCA AGT  
 921  
 Met Asp Met Cys Ser Phe Asp Thr Val Ala Arg Thr Ser Asp Ala Ser  
 260 265 270  
 25  
 CAG CTG TCA CCG TTC TGT CAA CTC TTC ACT CAC AAT GAG TGG AAG AAG  
 969  
 Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn Glu Trp Lys Lys  
 275 280 285 290  
 TAC AAC TAC CTT CAG TCC TTG GGC AAG TAC TAC GGC TAC GGC GCA GGC  
 1017  
 Tyr Asn Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly Tyr Gly Ala Gly  
 295 300 305  
 30  
 AAC CCT CTG GGA CCG GCT CAG GGG ATA GGG TTC ACC AAC GAG CTG ATT  
 1065  
 Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr Asn Glu Leu Ile  
 310 315 320  
 35  
 GCC CGG TTG ACT CGT TCG CCA GTG CAG GAC CAC ACC AGC ACT AAC TCG  
 1113  
 Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr Ser Thr Asn Ser  
 325 330 335  
 40  
 ACT CTA GTC TCC AAC CCG GCC ACC TTC CCG TTG AAC GCT ACC ATG TAC  
 1161  
 Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr Met Tyr  
 340 345 350  
 GTC GAC TTT TCA CAC GAC AAC AGC ATG GTT TCC ATC TTC TTT GCA TTG  
 1209  
 Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile Phe Phe Ala Leu  
 355 360 365 370  
 45  
 GGC CTG TAC AAC GGC ACT GAA CCC TTG TCC CGG ACC TCG GTG GAA AGC  
 1257  
 Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr Ser Val Glu Ser  
 375 380 385  
 50  
 GCC AAG GAA TTG GAT GGG TAT TCT GCA TCC TGG GTG GTG CCT TTC GGC  
 1305  
 Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val Val Pro Phe Gly  
 390 395 400

GCG CGA GCC TAC TTC GAG ACG ATG CAA TGC AAG TCG GAA AAG GAG CCT  
 1353  
 Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser Glu Lys Glu Pro  
 405 410 415  
 5  
 CTT GTT CGC GCT TTG ATT AAT GAC CGG GTT GTG CCA CTG CAT GGC TGC  
 1401  
 Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro Leu His Gly Cys  
 420 425 430  
 10  
 GAT GTG GAC AAG CTG GGG CGA TGC AAG CTG AAT GAC TTT GTC AAG GGA  
 1449  
 Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp Phe Val Lys Gly  
 435 440 445 450  
 15  
 TTG AGT TGG GCC AGA TCT GGG GGC AAC TGG GGA GAG TGC TTT AGT  
 1494  
 Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu Cys Phe Ser  
 455 460 465  
 TGAGATGTCA TTGTTATGCT ATACTCCAAT AGACCGTTGC TTAGCCATTG ACTTCACMTT  
 1554  
 20  
 GCTCGAACCG CCTGCCG  
 1571

## (2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 465 amino acids  
 25 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
 Met Val Thr Leu Thr Phe Leu Leu Ser Ala Ala Tyr Leu Leu Ser Gly  
 1 5 10 15  
 30 Arg Val Ser Ala Ala Pro Ser Ser Ala Gly Ser Lys Ser Cys Asp Thr  
 20 25 30  
 Val Asp Leu Gly Tyr Gln Cys Ser Pro Ala Thr Ser His Leu Trp Gly  
 35 40 45  
 35 Gln Tyr Ser Pro Phe Phe Ser Leu Glu Asp Glu Leu Ser Val Ser Ser  
 50 55 60  
 Lys Leu Pro Lys Asp Cys Arg Ile Thr Leu Val Gln Val Leu Ser Arg  
 65 70 75 80  
 40 His Gly Ala Arg Tyr Pro Thr Ser Ser Lys Ser Lys Tyr Lys Lys  
 85 90 95  
 Leu Val Thr Ala Ile Gln Ala Asn Ala Thr Asp Phe Lys Gly Lys Phe  
 100 105 110  
 Ala Phe Leu Lys Thr Tyr Asn Tyr Thr Leu Gly Ala Asp Asp Leu Thr  
 115 120 125  
 45 Pro Phe Gly Glu Gln Gln Leu Val Asn Ser Gly Ile Lys Phe Tyr Gln  
 130 135 140  
 Arg Tyr Lys Ala Leu Ala Arg Ser Val Val Pro Phe Ile Arg Ala Ser  
 145 150 155 160  
 50 Gly Ser Asp Arg Val Ile Ala Ser Gly Glu Lys Phe Ile Glu Gly Phe  
 165 170 175

Gln Gln Ala Lys Leu Ala Asp Pro Gly Ala Thr Asn Arg Ala Ala Pro  
 180 185 190  
 5 Ala Ile Ser Val Ile Ile Pro Glu Ser Glu Thr Phe Asn Asn Thr Leu  
 195 200 205  
 Asp His Gly Val Cys Thr Lys Phe Glu Ala Ser Gln Leu Gly Asp Glu  
 210 215 220  
 Val Ala Ala Asn Phe Thr Ala Leu Phe Ala Pro Asp Ile Arg Ala Arg  
 225 230 235 240  
 10 Ala Glu Lys His Leu Pro Gly Val Thr Leu Thr Asp Glu Asp Val Val  
 245 250 255  
 Ser Leu Met Asp Met Cys Ser Phe Asp Thr Val Ala Arg Thr Ser Asp  
 260 265 270  
 15 Ala Ser Gln Leu Ser Pro Phe Cys Gln Leu Phe Thr His Asn Glu Trp  
 275 280 285  
 Lys Lys Tyr Asn Tyr Leu Gln Ser Leu Gly Lys Tyr Tyr Gly Tyr Gly  
 290 295 300  
 20 Ala Gly Asn Pro Leu Gly Pro Ala Gln Gly Ile Gly Phe Thr Asn Glu  
 305 310 315 320  
 Leu Ile Ala Arg Leu Thr Arg Ser Pro Val Gln Asp His Thr Ser Thr  
 325 330 335  
 25 Asn Ser Thr Leu Val Ser Asn Pro Ala Thr Phe Pro Leu Asn Ala Thr  
 340 345 350  
 Met Tyr Val Asp Phe Ser His Asp Asn Ser Met Val Ser Ile Phe Phe  
 355 360 365  
 Ala Leu Gly Leu Tyr Asn Gly Thr Glu Pro Leu Ser Arg Thr Ser Val  
 370 375 380  
 30 Glu Ser Ala Lys Glu Leu Asp Gly Tyr Ser Ala Ser Trp Val Val Pro  
 385 390 395 400  
 Phe Gly Ala Arg Ala Tyr Phe Glu Thr Met Gln Cys Lys Ser Glu Lys  
 405 410 415  
 35 Glu Pro Leu Val Arg Ala Leu Ile Asn Asp Arg Val Val Pro Leu His  
 420 425 430  
 Gly Cys Asp Val Asp Lys Leu Gly Arg Cys Lys Leu Asn Asp Phe Val  
 435 440 445  
 40 Lys Gly Leu Ser Trp Ala Arg Ser Gly Gly Asn Trp Gly Glu Cys Phe  
 450 455 460  
 Ser  
 465

## (2) INFORMATION FOR SEQ ID NO: 7:

- 45 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 1567 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear
- 50 (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:

(A) NAME/KEY: CDS  
 (B) LOCATION:join(78..124, 177..1527)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

ACGTCCCAGG TCGGGGACTA CATCCGCTAT GTGGTCCTCT ACTTCGTCGG AAGAATATAAC  
 60

TGTCTCTTGT GGCTACC ATG GGG GTT TTC GTC GTT CTA TTA TCT ATC GCG  
 110  
 Met Gly Val Phe Val Val Leu Leu Ser Ile Ala  
 1 5 10

ACT CTG TTC GGC AG GTATGTGCAC CGCTCTAGGT TCAACTCGCC TGGTAACGTGA  
 164

Thr Leu Phe Gly Ser  
 15

CAAACAGCAC AG C ACA TCG GGC ACT GCG CTG GGC CCC CGT GGA AAT CAC  
 213  
 Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn His  
 20 25

AGC GAC TGC ACC TCA GTC GAC CGG GGG TAT CAA TGC TTC CCT GAG CTC  
 261  
 Ser Asp Cys Thr Ser Val Asp Arg Gly Tyr Gln Cys Phe Pro Glu Leu  
 30 35 40

TCC CAT AAA TGG GGT CTC TAC GCG CCC TAT TTC TCC CTC CAG GAT GAA  
 309

Ser His Lys Trp Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln Asp Glu  
 45 50 55 60

TCT CCG TTT CCT CTG GAC GTC CCG GAT GAC TGC CAC ATC ACC TTT GTG  
 357  
 Ser Pro Phe Pro Leu Asp Val Pro Asp Asp Cys His Ile Thr Phe Val  
 65 70 75

CAG GTG CTG GCC CGA CAT GGA GCG CGG TCT CCA ACC GAT AGC AAG ACA  
 405  
 Gln Val Leu Ala Arg His Gly Ala Arg Ser Pro Thr Asp Ser Lys Thr  
 80 85 90

AAG GCG TAT GCC GCG ACT ATT GCA GCC ATC CAG AAG AAT GCC ACC GCG  
 453  
 Lys Ala Tyr Ala Ala Thr Ile Ala Ala Ile Gln Lys Asn Ala Thr Ala  
 95 100 105

TTG CCG GGC AAA TAC GCC TTC CTG AAG TCG TAC AAT TAC TCC ATG GGC  
 501  
 Leu Pro Gly Lys Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser Met Gly  
 110 115 120

TCC GAG AAC CTG AAC CCC TTC GGG CGG AAC CAA CTG CAA GAT CTG GGC  
 549  
 Ser Glu Asn Leu Asn Pro Phe Gly Arg Asn Gln Leu Gln Asp Leu Gly  
 125 130 135 140

GCC CAG TTC TAC CGT CGC TAC GAC ACC CTC ACC CGG CAC ATC AAC CCT  
 597  
 Ala Gln Phe Tyr Arg Arg Tyr Asp Thr Leu Thr Arg His Ile Asn Pro  
 145 150 155

TTC GTC CGG GCC GCG GAT TCC TCC CGC GTC CAC GAA TCA GCC GAG AAG  
 645  
 Phe Val Arg Ala Ala Asp Ser Ser Arg Val His Glu Ser Ala Glu Lys  
 160 165 170

55

TTC GTC GAG GGC TTC CAA AAC GCC CGC CAA GGC GAT CCT CAC GCC AAC  
 693  
 Phe Val Glu Gly Phe Gln Asn Ala Arg Gln Gly Asp Pro His Ala Asn  
 175 180 185  
 5  
 CCT CAC CAG CCG TCG CCG CGC GTG GAT GTA GTC ATC CCC GAA GGC ACC  
 741  
 Pro His Gln Pro Ser Pro Arg Val Asp Val Val Ile Pro Glu Gly Thr  
 190 195 200  
 10  
 GCC TAC AAC AAC ACG CTC GAG CAC AGC ATC TGC ACC GCC TTC GAG GCC  
 789  
 Ala Tyr Asn Asn Thr Leu Glu His Ser Ile Cys Thr Ala Phe Glu Ala  
 205 210 215 220  
 15  
 AGC ACC GTC GGC GAC GCC GCG GCA GAC AAC TTC ACT GCC GTG TTC GCG  
 837  
 Ser Thr Val Gly Asp Ala Ala Asp Asn Phe Thr Ala Val Phe Ala  
 225 230 235  
 CCG GCG ATC GCC AAG CGT CTG GAG GCC GAT CTG CCC GGC GTG CAG CTG  
 885  
 Pro Ala Ile Ala Lys Arg Leu Glu Ala Asp Leu Pro Gly Val Gln Leu  
 240 245 250  
 20  
 TCC GCC GAC GAC GTG GTC AAT CTG ATG GCC ATG TGT CCG TTC GAG ACG  
 933  
 Ser Ala Asp Asp Val Val Asn Leu Met Ala Met Cys Pro Phe Glu Thr  
 255 260 265  
 25  
 GTC AGC CTG ACC GAC GAC GCG CAC ACG CTG TCG CCG TTC TGC GAC CTC  
 981  
 Val Ser Leu Thr Asp Asp Ala His Thr Leu Ser Pro Phe Cys Asp Leu  
 270 275 280  
 30  
 TTC ACC GCC GCC GAG TGG ACG CAG TAC AAC TAC CTG CTC TCG CTG GAC  
 1029  
 Phe Thr Ala Ala Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser Leu Asp  
 285 290 295 300  
 Lys Tyr Tyr Gly Tyr Gly Gly Asn Pro Leu Gly Pro Val Gln Gly  
 305 310 315  
 35  
 GTG GGC TGG GCG AAC GAG CTG ATC GCG CGG CTG ACG CGC TCC CCC GTC  
 1125  
 Val Gly Trp Ala Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val  
 320 325 330  
 CAC GAC CAC ACC TGC AAC AAC ACC CTC GAC GCC AAC CCG GCC ACC  
 1173  
 His Asp His Thr Cys Val Asn Asn Thr Leu Asp Ala Asn Pro Ala Thr  
 335 340 345  
 40  
 TTC CCG CTG AAC GCC ACC CTC TAC GCG GAC TTT TCG CAC GAC AGT AAC  
 1221  
 Phe Pro Leu Asn Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Ser Asn  
 350 355 360  
 45  
 CTG GTG TCG ATC TTT TGG GCG CTG GGT CTG TAC AAC GGC ACC AAG CCC  
 1269  
 Leu Val Ser Ile Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro  
 365 370 375 380  
 50  
 CTG TCG CAG ACC ACC GTG GAG GAT ATC ACC CGG ACG GAC GGG TAC GCG  
 1317  
 Leu Ser Gln Thr Thr Val Glu Asp Ile Thr Arg Thr Asp Gly Tyr Ala  
 385 390 395

5                   GCC GCC TGG ACG GTG CCG TTT GCC GCC CGC GCC TAC ATC GAG ATG ATG  
 1365               Ala Ala Trp Thr Val Pro Phe Ala Ala Arg Ala Tyr Ile Glu Met Met  
 400               405               410  
 10                  CAG TGT CGC GCG GAG AAG CAG CCG CTG GTG CGC GTG CTG GTC AAC GAC  
 1413               Gln Cys Arg Ala Glu Lys Gln Pro Leu Val Arg Val Leu Val Asn Asp  
 415               420               425  
 15                  CGT GTC ATG CCG CTG CAC GGC TGC GCG GTG GAT AAT CTG GGC AGG TGT  
 1461               Arg Val Met Pro Leu His Gly Cys Ala Val Asp Asn Leu Gly Arg Cys  
 430               435               440  
 20                  AAA CGG GAC GAC TTT GTG GAG GGA CTG AGC TTT GCG CGG GCA GGA GGG  
 1509               Lys Arg Asp Asp Phe Val Glu Gly Leu Ser Phe Ala Arg Ala Gly Gly  
 445               450               455               460  
 25                  AAC TGG GCC GAG TGT TTC TGATGTACAT GCTGTAGTTA GCTTTGAGTC  
 1557               Asn Trp Ala Glu Cys Phe  
 465  
 30                  CTGAGGTACC  
 1567

## (2) INFORMATION FOR SEQ ID NO: 8:

25                  (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 466 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear  
 (ii) MOLECULE TYPE: protein  
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:  
 30                  Met Gly Val Phe Val Val Leu Leu Ser Ile Ala Thr Leu Phe Gly Ser  
 1                   5                   10                   15  
 Thr Ser Gly Thr Ala Leu Gly Pro Arg Gly Asn His Ser Asp Cys Thr  
 20               25                   30  
 35                  Ser Val Asp Arg Gly Tyr Gln Cys Phe Pro Glu Leu Ser His Lys Trp  
 35               40                   45  
 Gly Leu Tyr Ala Pro Tyr Phe Ser Leu Gln Asp Glu Ser Pro Phe Pro  
 50               55                   60  
 Leu Asp Val Pro Asp Asp Cys His Ile Thr Phe Val Gln Val Leu Ala  
 65               70                   75                   80  
 Arg His Gly Ala Arg Ser Pro Thr Asp Ser Lys Thr Lys Ala Tyr Ala  
 85               90                   95  
 Ala Thr Ile Ala Ala Ile Gln Lys Asn Ala Thr Ala Leu Pro Gly Lys  
 100              105                   110  
 45                  Tyr Ala Phe Leu Lys Ser Tyr Asn Tyr Ser Met Gly Ser Glu Asn Leu  
 115               120                   125  
 Asn Pro Phe Gly Arg Asn Gln Leu Gln Asp Leu Gly Ala Gln Phe Tyr  
 130               135                   140  
 50                  Arg Arg Tyr Asp Thr Leu Thr Arg His Ile Asn Pro Phe Val Arg Ala  
 145               150                   155                   160  
 Ala Asp Ser Ser Arg Val His Glu Ser Ala Glu Lys Phe Val Glu Gly

	165	170	175
5	Phe Gln Asn Ala Arg Gln Gly Asp Pro His Ala Asn Pro His Gln Pro 180	185	190
	Ser Pro Arg Val Asp Val Val Ile Pro Glu Gly Thr Ala Tyr Asn Asn 195	200	205
10	Thr Leu Glu His Ser Ile Cys Thr Ala Phe Glu Ala Ser Thr Val Gly 210	215	220
	Asp Ala Ala Ala Asp Asn Phe Thr Ala Val Phe Ala Pro Ala Ile Ala 225	230	235
15	Lys Arg Leu Glu Ala Asp Leu Pro Gly Val Gln Leu Ser Ala Asp Asp 245	250	255
	Val Val Asn Leu Met Ala Met Cys Pro Phe Glu Thr Val Ser Leu Thr 260	265	270
20	Asp Asp Ala His Thr Leu Ser Pro Phe Cys Asp Leu Phe Thr Ala Ala 275	280	285
	Glu Trp Thr Gln Tyr Asn Tyr Leu Leu Ser Leu Asp Lys Tyr Tyr Gly 290	295	300
25	Tyr Gly Gly Asn Pro Leu Gly Pro Val Gln Gly Val Gly Trp Ala 305	310	315
	Asn Glu Leu Ile Ala Arg Leu Thr Arg Ser Pro Val His Asp His Thr 325	330	335
30	Cys Val Asn Asn Thr Leu Asp Ala Asn Pro Ala Thr Phe Pro Leu Asn 340	345	350
	Ala Thr Leu Tyr Ala Asp Phe Ser His Asp Ser Asn Leu Val Ser Ile 355	360	365
35	Phe Trp Ala Leu Gly Leu Tyr Asn Gly Thr Lys Pro Leu Ser Gln Thr 370	375	380
	Thr Val Glu Asp Ile Thr Arg Thr Asp Gly Tyr Ala Ala Ala Trp Thr 385	390	395
40	Val Pro Phe Ala Ala Arg Ala Tyr Ile Glu Met Met Gln Cys Arg Ala 405	410	415
	Glu Lys Gln Pro Leu Val Arg Val Leu Val Asn Asp Arg Val Met Pro 420	425	430
45	Leu His Gly Cys Ala Val Asp Asn Leu Gly Arg Cys Lys Arg Asp Asp 435	440	445
	Phe Val Glu Gly Leu Ser Phe Ala Arg Ala Gly Gly Asn Trp Ala Glu 450	455	460
50	Cys Phe 465		

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**Claims**

1. A process for the production of a modified phytase with improved activity properties characterized therein that the

following steps are effected:

- 5        a) the three dimensional structure of the phytase to be modified and, optionally of another phytase with activity properties which are more favorable than the ones of the phytase to be modified is/are computer modelled on the basis of the three dimensional structure of the phytase of *Aspergillus niger*;
  - 10      b) the structure of the active sites of the phytase to be modified and of the phytase with the more favorable activity properties are compared and those amino acid residues in both active sites which are different are identified;
  - 15      c) a DNA sequence coding for a modified phytase is constructed by changing the nucleotides coding for at least one of the amino acids by which both active sites differ;
  - 20      d) integrating such a DNA sequence into a vector capable of expression in a suitable host cell;
  - 25      e) transforming a suitable host cell by the DNA sequence of c) or the vector of d), growing said host cell under suitable growth conditions and isolating the modified phytase from the host cell or the culture medium by methods known in the state of the art.
- 20      2. A process as claimed in claim 1 wherein the phytase to be modified is of eukaryotic origin.
3. A process as claimed in claim 1 or 2 wherein the phytase to be modified is of fungal origin.
4. A process as claimed in any one of claims 1 to 3 wherein the phytase to be modified is of *Aspergillus* origin.
- 25      5. A process as claimed in any one of claims 1 to 4 wherein the phytase to be modified is a phytase from *Aspergillus fumigatus*.
- 30      6. A process as claimed in any one of claims 1 to 5 wherein the phytase with the more favorable activity properties is of eukaryotic origin.
7. A process as claimed in any one of claim 1 to 6 wherein the phytase with the more favorable activity properties is of fungal origin.
- 35      8. A process claimed in any one of claims 1 to 7 wherein the phytase with the more favorable activity properties is of *Aspergillus* origin.
9. A process as claimed in any one of claims 1 to 8 wherein the phytase with the more favorable activity properties is a phytase from *Aspergillus terreus*.
- 40      10. A process as claimed in any one of claims 1 to 9 wherein the phytase to be modified is a phytase of *Aspergillus fumigatus* and the phytase with the more favorable activity properties is the *Aspergillus niger* phytase.
- 45      11. A process as claimed in any one of claims 1 to 9 wherein the phytase to be modified is a phytase of *Aspergillus fumigatus* and the phytase with the more favorable activity properties is the *Aspergillus terreus* phytase.
- 50      12. A modified phytase obtained or obtainable by a process as claimed in any one of claims 1 to 11.
13. A phytase which has been modified in a way that its activity property is more favorable than the one of the non-modified phytase.
- 55      14. A phytase according to claim 13 characterized therein that the amino acid sequence of the non-modified phytase has been changed by deletion, substitution and/or addition by one or more amino acids.
15. A phytase according to any one of claims 13 or 14 wherein changes have been made at at least one position which is homologous to one of the following positions of the amino acid sequence of the phytase of *Aspergillus niger*: 27, 66, 71, 103, 140, 141, 188, 205, 234, 235, 238, 274, 277, 282, 340 and/or 424, preferably 27, 66, 140, 205, 274, 277, 282 and/or 340.

16. A phytase according to any one of claims 13 to 15 which is the phytase of *Aspergillus*, preferably *Aspergillus fumigatus*.
17. A phytase according to any one of claims 15 or 16 wherein at position 27 or at least at position 27 a change occurs.
- 5 18. A phytase according to claim 17 wherein the amino acid at position 27 is replaced by one selected from one of the following groups:
  - a) Ala, Val, Leu, Ile; or
  - 10 b) Thr.
19. A phytase according to claim 17 or 18 wherein in addition to position 27 a change occurs also at position 66.
- 15 20. A phytase according to claim 17 or 18 wherein in addition to position 27 a change occurs also at position 140.
21. A phytase according to any one of claims 13 to 20 which is characterized by at least one of the following mutations: Q27L, Q27N, Q27T, Q27I, Q27V, Q27A, Q27G, S66D, S140Y, D141G, A205E, Q274L, G277D, G277K, Y282H and/or N340S.
- 20 22. A DNA sequence comprising a DNA sequence coding for a phytase as claimed in any one of claims 12 to 21.
23. A vector comprising the DNA sequence of claim 22.
- 25 24. The vector of claim 23 which is an expression vector.
25. A host cell which has been transformed by a DNA sequence as claimed in claim 22 or the vector of claim 23 or 24.
- 30 26. A process for the preparation of a phytase as claimed in any one of claims 12 to 21 wherein the host cell as claimed in claim 25 is cultured under suitable culture conditions and the phytase is isolated from such host cells or the culture medium by methods known in the art.
27. A food or feed composition comprising a phytase as claimed in any one of claims 12 to 21.

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**Figure 1**

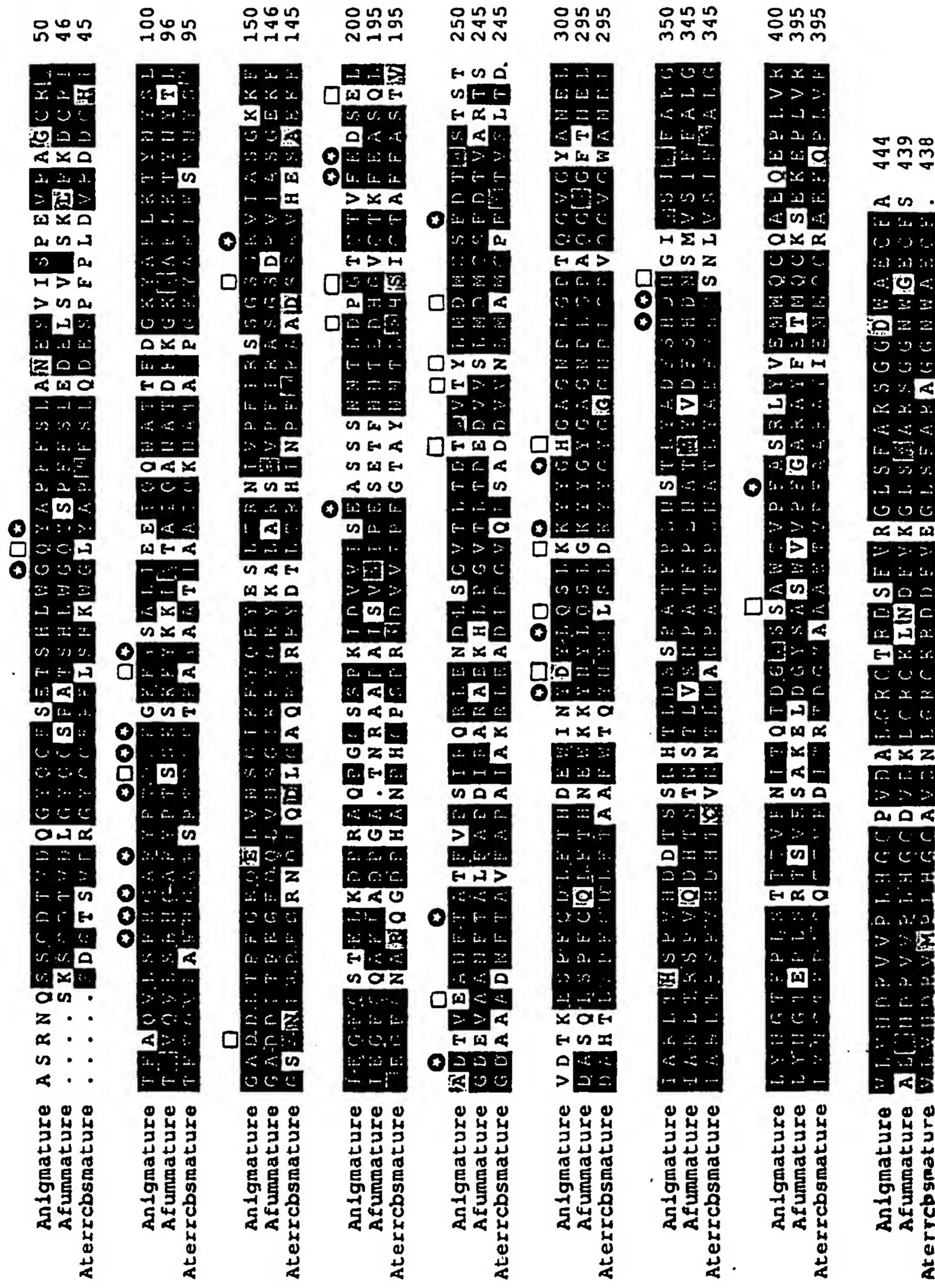


Figure 2

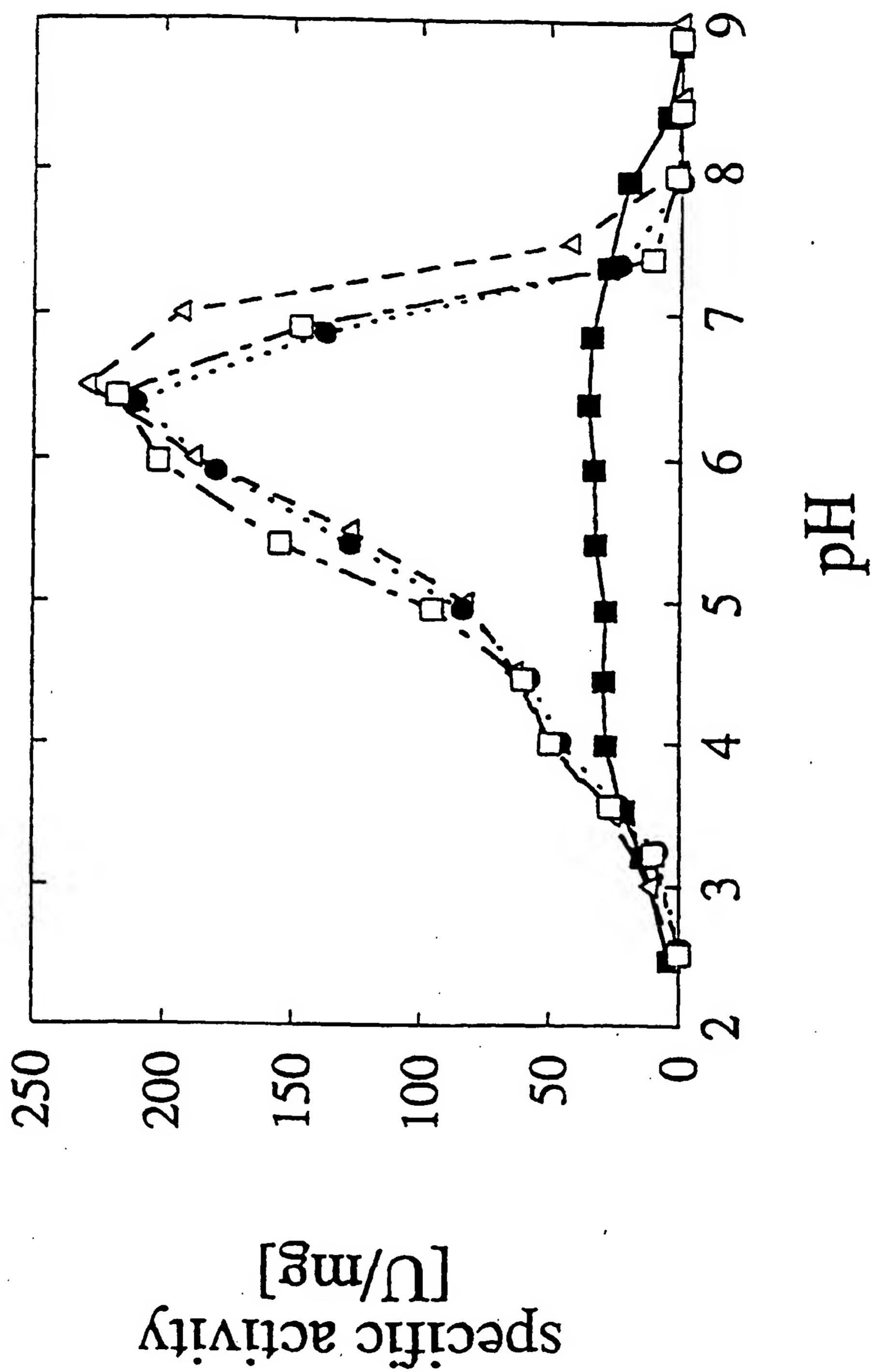


Figure 3

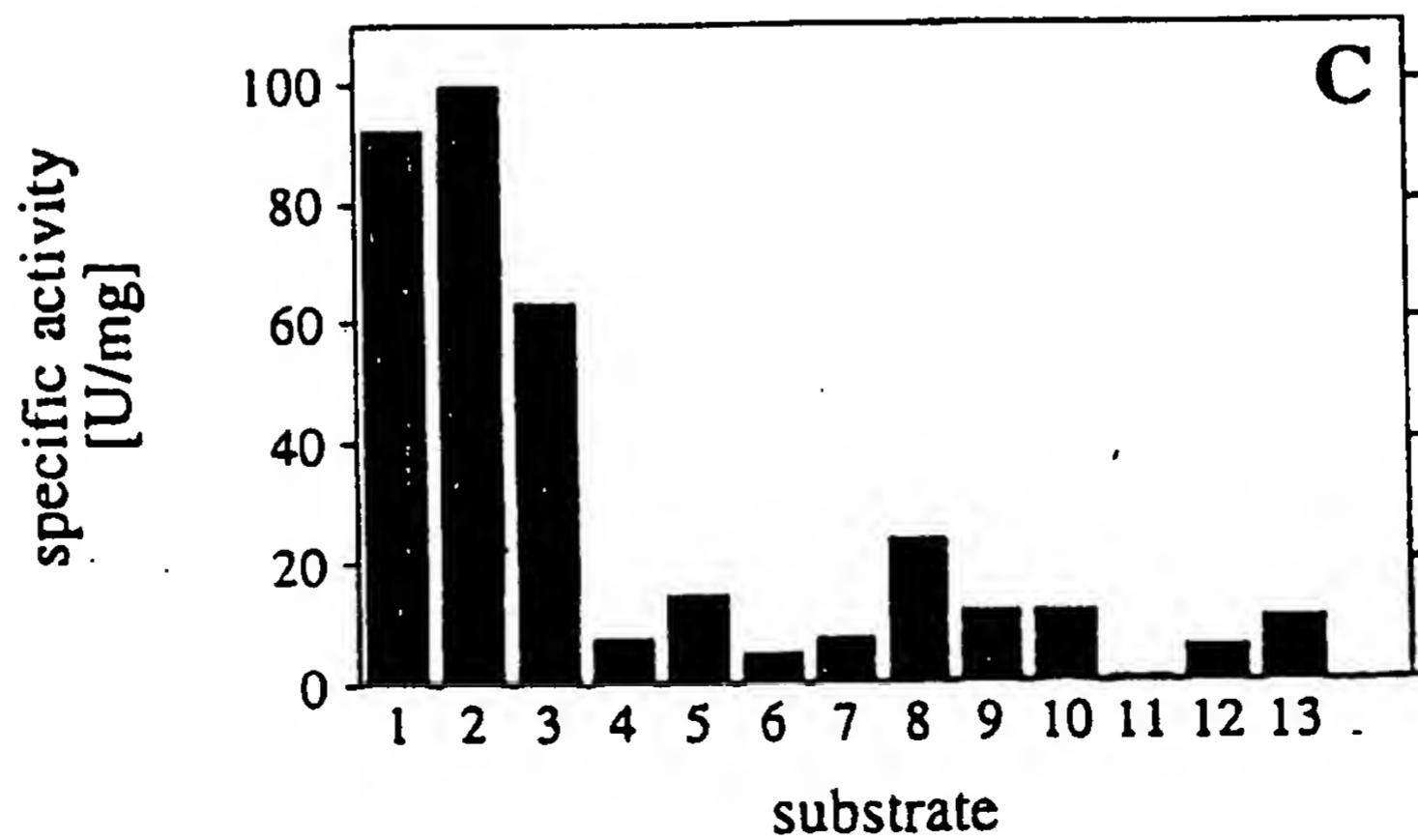
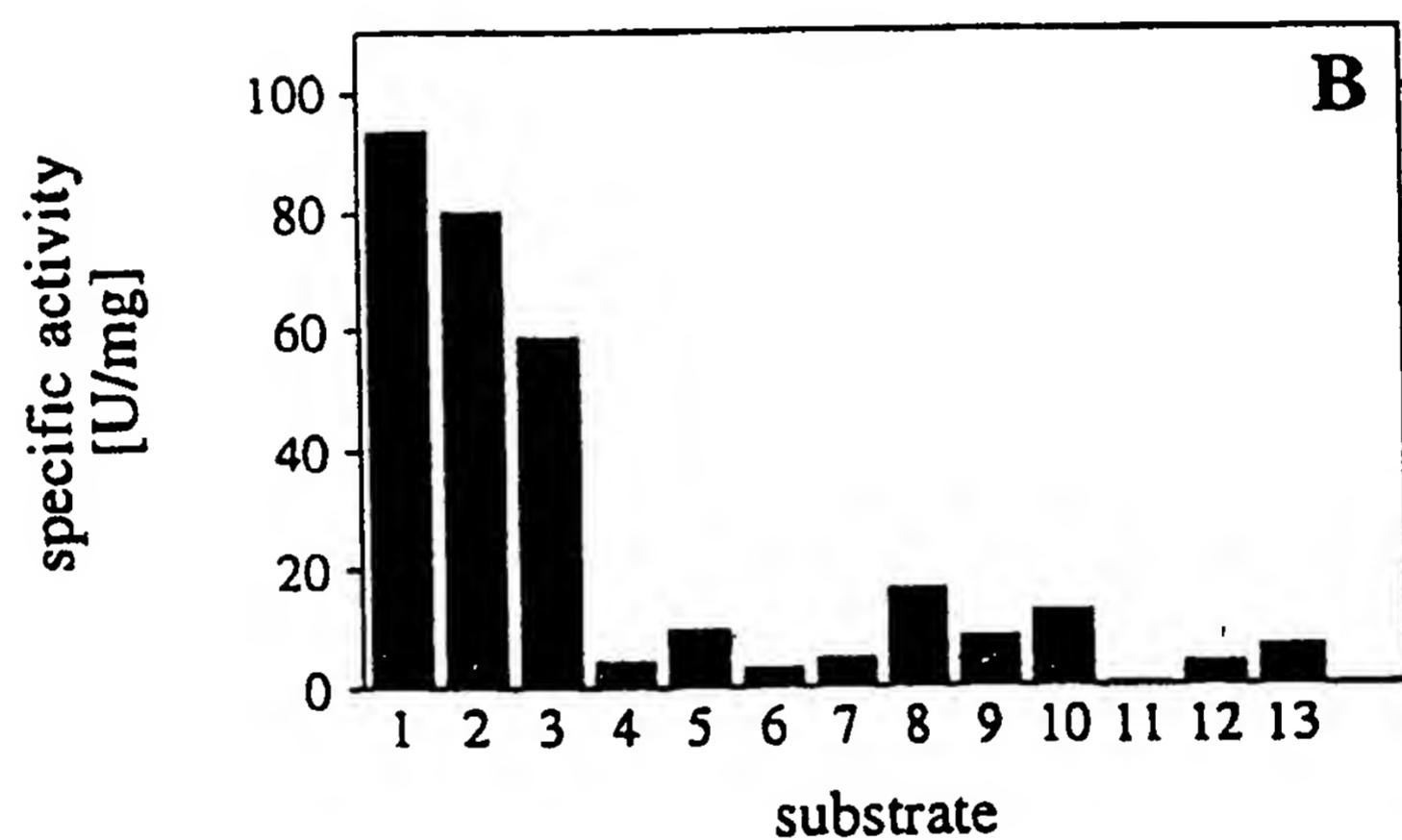
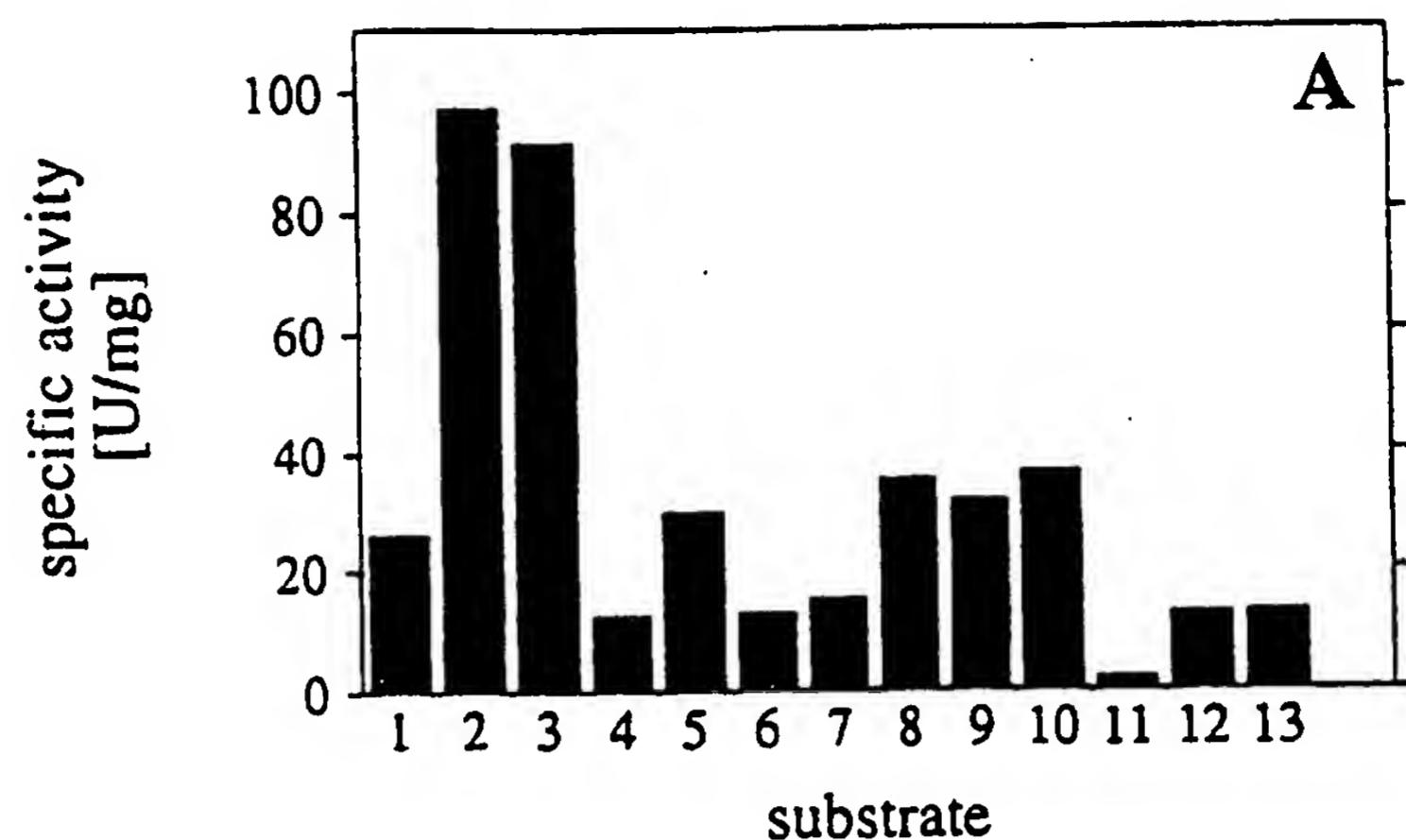


Figure 4/1

1 TCTGTAAACCGATAGCGGACCGACTAGGCATCGTGTGATCCACAATACTCA 50  
 .  
 51 GACAATGCAACTCAGTCGAATATGAAGGGCTACAGCCAGCATTAAATAC 100  
 .  
 101 GGCGTCTAGGTGGCTCCGGATGAGGAGGAGGAGGCTCGTGTTCAT 150  
 .  
 151 TTGGTCACTGGCTTTTCACGGTCGCTCTTCGCTTATTACTTGCTAT 200  
     M A F F T V A L S L Y Y L L S 15  
 .  
 201 CGAGgtgagatcccccacaaatacctgtccgtttagttggaaatcggcacccat 250  
     R 16  
 .  
 251 cegacacaçAGTCTCTGCTCAGGCCCAAGTGGTCCAGAATCATGCAA 300  
     V S A Q A P V V Q N H S C N 30  
     +  
 .  
 301 TACGGCCGACGGTGGATATCAATGCTTCCCCAATGTCCTCATGTTGGG 350  
     T A D G G Y Q C F P N V S K V W G 47  
     +  
 .  
 351 GTCAGTACTCGCCGTACTTCTCCATCGAGCACGGACTCAGCTATCTTGAG 400  
     Q Y S P Y F S I E Q E S A I S E 63  
 .  
 401 GACGTGCCCTATGGCTGGAGGTACCTTGTGCAGGTGGCTCTGGCGCA 450  
     D V P K G C E V T F V Q V L S R K 80  
 .  
 451 TCGGGCTACGTATCCGACAGAGTCGAAGAGTAAGGCGTACTCGGGTTGA 500  
     G A R Y P T E S K S K A Y S G L I 97  
 .  
 501 TTGAACCAATCCAGAAGAACTACCTCTTTGGGACAGTATGCTTT 550  
     E A I Q K N A T S F W G Q Y A F 113  
     +  
 .  
 551 CTGGAGAGTTATAACTATACCTCTGGCGCGGATGACTTGAATCTTCGG 600  
     L E S Y N Y T L G A D D L T I F G 130  
     +  
 .  
 601 CGAGAACCAAGATGGTTGATTGGGTGCCAAGTTCTACCGACGGTATAAGA 650  
     E N Q M V D S G A K F Y R R Y K N 147  
 .  
 651 ATCTCGCCAGGAAAAATACTCTTTATCCGTGCATCAGGCTGACCGT 700  
     L A R K N T P F I R A S G S D R 153

Figure 4/2

701 GTCGTTGGCTCTGGGGAGAAGTCATTAATGGATTCCAAAGGCTCAGCT 750  
 V V A S A E K F I N G F R K A Q L 180  
 . . . .  
 751 CCACGGACCATGGCTCCAAACGTGCTACGCCAGTTGTCAATGTGATTATCC 800  
 K D H G S K R A T P V V N V I I P 197  
 . . . .  
 801 CTGAAATCGATGGTTAACAAACCCCTGGACCATACCAACGTGGCTATCT 850  
 E I D G F N N T L D K S T C V S 213  
 +  
 . . . .  
 851 TTGAGAAATGATGAGCGGGCGGATGAAATTGAAGCCAATTTCACGGCAAT 900  
 F E N D E R A D E I E A N F T A I 230  
 +  
 . . . .  
 901 TATGGGACCTCCGATCCGCAAACGTCGGAAAATGACCTCCCTGGCATCA 950  
 M G P P I R K R L E N D L P G I K 247  
 . . . .  
 951 AACTTACAAACGAGAAATGTAATATAATTGATGGATAATGTGCTCTTCGAC 1000  
 L T N E N V I Y L M D M C S F D 263  
 . . . .  
 1001 ACCATGGCGGCACCGCCCACGGAAACCGAGCTGCTCCATTTTGCCAT 1050  
 T M A R T A K G T E L S P F C A I 280  
 . . . .  
 1051 CITCACTGAAAAGGAGCTGGCTGGCACTACGGACTACCCTCAATCTCTATCAA 1100  
 F T E K E W L Q Y D Y L Q S L S K 297  
 . . . .  
 1101 AGTACTACGGCTACGGTGGGAAGCCCCCTGGCCAGCTCAGGGAAAT 1150  
 Y Y G Y G A G S P L G P A Q G I 313  
 . . . .  
 1151 GGCTTCACCAACGAGCTGATTGCCCGACTAACGCAATGCCCGTCCAGGA 1200  
 G F T N E L I A R L T Q S P V Q D 330  
 . . . .  
 1201 CAACACAAGCACCAACCACACTCTAGACTCGAACCCAGCCACATTCCGC 1250  
 N T S T N H T L D S N P A T F P L 347  
 + +  
 . . . .  
 1251 TCGACAGGAAGCTCTACGCCGACTTCTCCACGGACAATAGCATGATAATCG 1300  
 D R K L Y A D F S H D N S M I S 363  
 . . . .  
 1301 ATATTCTCGCCATGGCTCTACAAACGGCACCCAGCCGCTGTCAATGGA 1350  
 I F F A M G L Y N G T Q P L S M D 380  
 +  
 . . . .

Figure 4/3

1351 TTCCGTGGAGTCGATCCACGGAGATGGACGGTTACGCCGGTCTTGGACTG 1400  
 S V E S I Q E M D G Y A A S W T V 397

1401 TTCCGTTGGTGCAGGGCTTACTTGAGCTCATGCAGTGCAGAAGAAG 1450  
 P F G A R A Y F E L M Q C E K K 413

1451 GAGCCGCTTGTGCGGGTATTAGTGAATGATCGCGTTGTTCTCTCATGG 1500  
 E P L V R V L V N D R V V P L H G 430

1501 CTGGCGAGTTGACAAGTTGGACGGTGCACCTTGGACCAATTGGTAGAGG 1550  
 C A V D K F G R C T L D D W V E G 447

1551 CCTTGAATTTCGAAGGAGCGCCGGAACTCGAACACTTGTACCTTA 1600  
 L N F A R S G G N W K T C F T L 463

1601 TAAAGGGCTTGTCTCATTCTAAAGTGTGTGCAGGTATAGGAAGGTAG 1650

1651 CGAATTAGCTGTTGGCTTACTCTTATTAGACCAAGAACATTGATTGTIG 1700

1701 TTCTCAAGGCCTCTAGCATATCGTCAAGTGGATAATCACCTATCCTC 1750

1751 CATGTGTAGGTGAACCCGCTTGGCATCACCTCTGTGTTCAAGACTAG 1800

1801 TTTCACCAAACATATCCTCGTGCTCTCTCTGCTCTGGCTCATAT 1850

1851 TACACTGTCTCTATCTATATCGTCAACAAAACCTACCAACCCAAACCAA 1900

1901 ATGTCACACTTCCAGCACGAAATTCTTCG 1931

Figure 5/1

1	TTCCACGGCTGAAAGCCTGACTGCGATTCCAAGCTGCATGCAGGCTGCTC	50
51	AACTGCCTGCTTATCTTCATCAGACCGCAGATACACAACCTGGTCTGTAGA	100
101	TGCACCCATGACGGACGAACGGACCGCTCTCTGGCCTCCAGGGACCCGG	150
151	AGGTCGAGGGCGATGAGGTGGGCCCCCTCGACGGCCTCCCAGTCCCTGTTG	200
201	CAGTTGAGATCTCGCTGCGAACGTCGACCGCAGATATGGTTGTCTTCGAC	250
251	GTTTCTCGCTTCGAGGAAGAATTGCTGCTGTGACGGATGAGTCCTGTTGT	300
	M S L L L	5
301	TGCTGGTGCCTGTCGGCGGGTTGGTCGGTTATAgcaacgtccccccccc	350
	L V L S G G L V A L Y	16
351	tggcacatcgtccccccgcacgtccccacaaacgaagTGTCCTCAAGAA	400
	V S R N	20
401	ATCCGCATGTTGATAAGCCACTCTTGCATAACAGTGGAAAGGAGGGTATCAG	450
	P H V D S K S C N T V E G G Y Q	36
451	TGTCGTCCAGAAAATCTCCACTCCTGGGGCCAGTATTCTCCATTCTTC	500
	C R P E I S K S W G Q Y S P F F S	53
501	CCTGGCAGACCAGTCGGAGATCTGCCAGATGTCCACAGAACTGCAAGA	550
	L A D Q S E I S P D V P Q N C K I	70
551	TTACGTTGTCAGCTGCTTCTCGTCACGGCGCTAGATAACCTACGTCT	600
	T F V Q L L S R H G A R Y P T S	86
601	TCCAAAGACGGACCTGTATTGGAGCTGATCAGTCGGATTCAAGAAAGACGGC	650
	S K T E L Y S Q L I S R I Q K T A	103
651	GAATGGCTACAAAGGCTACTATGCCTTCTGAAAGACTACAGATAACCAAC	700
	T A Y K G Y Y A F L K D Y R Y Q L	120
701	TGGGAGCGAACGACCTGACGCCCTTGGGAAAAACAGATGATCCAGTTG	750
	G A N D L T P F G E N Q M I Q L	136

Figure 5/2

751 GGCATCAAGTTTATAACCAATTACAAGAGTCCTGCCAGGAATGCCGTCCC 800  
 G I K F Y N H Y K S L A R N A V P 153

801 ATTGTTCTGTTGCTCCGGCTCTGATCGGGTCAATTCCCTCGGGGAGACTTT 850  
 F V R C S G S D R V I A S G R L F 170

851 TCATCGAACGTTTCCAGAGGCCAAAGTGCTGGATCCTCAATTAGACAAAG 900  
 I E G F Q S A K V L D P K S D K 186

901 CATGACCGCTCCTCCCACGATCACGTGATCATCGAGGAGGGTCCGTCTTA 950  
 H D A P P T I N V I I E E G P S Y 203

951 CAATAACACGCTCGACACCGGCAGCTGTCCAGTCTTGAGGACAGCAGCG 1000  
 N N T L D T G S C P V F E D S S G 220  
 +

1001 GGGGACATGACGGCACAGGAAAAGTCGCAAGCAATTGGCACCGCTATC 1050  
 G H D A Q E K F A K Q F A P A I 236

1051 CTGGAAAAGATCAAGGACCATCTTCCCCGGTGGACCTGGCCGTGTGGA 1100  
 L E K I K D H L P G V D L A V S D 253

1101 TGTACCGTACTTGATGGACTTGIGICCGTTTGAGACCTTGGCTCGCAACC 1150  
 V P Y L M D L C P F E T L A R N H 270  
 +

1151 ACACAGACACGGCTGCTCGGTTCTGGCTCTTCCACCGAAGAGGAGTGG 1200  
 T D T L S P F C A L S T Q E E W 286

1201 CAGGCATAATGACTACTACCAAAAGTCGGGAAATACTATGGCAATGGCGG 1250  
 Q A Y D Y Y Q S L G K Y Y G N G G 303

1251 GGGTAACCGTGGGGCCAGCCCAAGGGTGGGTTTGTCACGAGTTGA 1300  
 G N P L G P A Q G V G F V N E L I 320

1301 TTGCTCCATGACCCATAGCCCTGTCCAGGACTACACCACGGTCAACCAC 1350  
 A R M T H S P V Q D Y T T V N H 336  
 +

1351 ACTCTTGACTCGAATCCGGGACATTCCTTGAACGGGACGCTGTACGC 1400  
 T L D S N P A T F P L N A T L Y A 353  
 +

Figure 5/3

1401 AGATTCAGCCACCGACAACACAATGACGTCAATTTCGGCGGCCCTGGGCC 1450  
 O F S K D N T M T S I F A A L G L 370

1451 TGTACACGGCACCGCGAACGCTGTCCACCGACCGAGATCAAAGTCCATTGAA 1500  
 Y N G T A K L S T T E I K S I E 386  
 +

1501 GAGACGGACGGCTACTCGGGGGCGTGGACCGCTCCGTTGGGGGGGGAGC 1550  
 E T D G Y S A A W T V P F G G R A 403

1551 CTATATCGAGATGATGCAGTGTGATGATTGGATGAGCCAGTCGTTGGG 1600  
 Y I E M M Q C D D S D E P V V R V 420

1601 TGCTGGTCAACGACCGGGTGTTGCCACTTGCACTGGCTGGAGGTGGACTCC 1650  
 L V N D R V V P L H G C E V D S 436

1651 CTGGGGCGATGCCAACGAGACGGACTTGTCAAGGGACTGAGTTTGCGCG 1700  
 L G R C K R D D F V R G L S F A R 453

1701 ACAGGGTGGGAACGGGGGGTGTACGGCTGGCTTGAGTAGGTTATT 1750  
 Q G G N W E G C Y A A S E \* 466

1751 CAGCGAGTTTGGACCTTCTATCCTCAAACACTGCACAAAAGACACACTG 1800

1801 CATGAAATGGTACAGGCCCTGGAGCGTTTAGAAGGAAAAAGTT 1845

Figure 6/1

1	AGATTCAACGACGGAGGAATCGCAACCCTAATTGTCGGTATCATGGTGAC	50
	M V T	3
51	TCTGACTTTCTGCTTTCGGCCGGGTATCTGCTTTCTGGgtggatggccc	100
	L T F L L S A A Y L L S G	16
101	ggacccatcgcccgataggccgccccggacccctgaaacggagTAGA	150
	R	17
151	GTTGCTGGGCACCTAGTTCTGCTGGCTCCAAGTCCCTCGATAACGGTAGA	200
	V S A A P S S A G S K S C D T V D	34
201	CCTCCGGTACCAAGTGCCTCCCTGCCACTTCTCATCTATGGGCCAGTACT	250
	L G Y Q C S P A T S H L W G Q Y S	51
251	CGCCATTCTTTCGCTCGAGGACGGAGCTGTCCGTGTCAAGTAAGCTTCCC	300
	P F F S L E D E L S V S S K L P	67
301	AAGGATTGCCGGATCACCTGGTACAGGTGCTATGCCCATGGAGCGCG	350
	K D C R I T L V Q V L S R H G A R	84
351	GTACCCAAACGCTCAAGAGCAAAAGTATAAGAACGTTGTGACGGCGA	400
	Y P T S S K S K K Y K K L V T A I	101
401	TCCAGGCCAATGCCACCGACTCAAGGGCAAGTTGCCCTTTGAAGACG	450
	Q A N A T D F K G K F A F L K T	117
	*	
451	TACAACATACTCTGGTGGGATGACCTCACTCCCTTGGGGAGCAGCA	500
	Y N Y T L G A D D L T P F G E Q Q	134
	*	
501	GCTGGTGAACCTGGGCATCAAGTCTACCAAGGGTACAAGGCTCTGGCGC	550
	L V N S G I K F Y Q R Y K A L A R	151
	*	
551	GCAGTGTGGTGGCTTATTGGCGCTCAAGGCTGGACCGGGTTATTGCT	600
	S V V P F I R A S G S D R V I A	167

Figure 6/2

601	TCGGGAGAGAAGTTCATCGACGGGTCCAGCAGGCCAGCTGGCTGATCC S G E K F I E G F Q Q A K L A D P	650 184
651	TGGGGGACGAACCGCGCCGCTCCGGCGATTAGTGTGATTATTCCGGAGA G A T N R A A P A I S V I I P E S	700 201
701	GCGAGACGTTCAACAATAACGCTGGACCACCGTGTGCGAACGAAAGTTGAG E T F N N T L D H G V C T K F E +	750 217
751	GCGAGTCAGCTGGAGATGAGGTTGGCCAAATTCACTGCGCTCTTGC A S Q L G D E V A A N F T A L F A +	800 234
801	ACCCGACATCCGAGCTCGCGCCGAGAACCATCTTCTGGCGTACGCTGA P D I R A R A E K H L P G V T L T	850 251
851	CAGACGGAGGACGTTGTCAGTCTAAATGGACATGTGTTGTTGATA <u>ACGGTA</u> D E D V V S L M D M C S F D T V	900 257
901	<u>GCGCGCACCAAGGACGGCAACTCAGCTGTCAACCGTTCTGTCAACTCTTCAC</u> A R T S D A S Q L S P F C Q L F T	950 284
951	<u>TCACAAATTGAGTGGAGAAGTACAACCTACCTTCAGTCCTTGGCAAGTACT</u> K N E W K K Y N Y L Q S L G K Y Y	1000 301
1001	ACGGCTACGGGGAGGCAACCCCTCTGGGACCCGGCTCAGGGATACGGTTG G Y G A G N P L G P A Q G I G F	1050 317
1051	ACCAACGGAGCTGATTGCCCGTTGACTCGTCGCCAGTCAGGACCAAC T N E L I A R L T R S P V Q D H T	1100 334
1101	CAGCACTAACTCGACTCTAGTCTCCAACCCGGCACCTTCCCGTTGAACG S T N S T L V S N P A T F P L N A +	1150 351
1151	CTACCATGTACGTCGACTTTCACACGGACAACAGGATGGTTCCATCTTC T M Y V D F S K D N S M V S I F	1200 357
1201	TTTGCATGGGCCTGTACACGGCACTGAACCCCTGTCGGACCTCGGT F A L G L Y N G T E P L S R T S V	1250 384

Figure 6/3

1251 GGAAAGGCCAAGGAATTGGATGGTATTCTGCATCCTGGTGTCCTT 1300  
 E S A K E L D G Y S A S W V V P F 401

1301 TCGGGCGCCGAGCCTACTTCGAGACGATGCAATGCAAGTCGGAAAAGGAG 1350  
 G A R A Y F E T M Q C K S E K E 417

1351 CCTCTTGTTCGGCTTTGATTAATGACCGGTTCTGCCACTGCATGGCTG 1400  
 P L V R A L I N D R V V P L K G C 434

1401 CGATGTGGACAAGCTGGGGGATGCAAGCTGAATGACTTTGTCAAGGGAT 1450  
 D V D K L G R C K L N D F V K G L 451

1451 TGAGTTGGCCAGATCTGGGGCAACTGGGGAGAGTGCTTAGTTGAGAT 1500  
 S W A R S G G N W G E C F S 465

1501 GTCATTGTTATGCTATACTCCAATAGACCGTTGCTTAGCCATTCACTTC 1550

1551 CTTTGCTCGAACCGCCCTGCCG 1571

Figure 7/1

1	ACGTCCCAGTCGGGACTACATCCGCTATGTGGTCTCTACTTCGTGG	50
51	AAGAATAACTGTCTCTTGCGCTACCATGGGGTTTCGTGGTCTATT	100
	M G V F V V L L	8
101	ATCTATCGGACTCTGTTGGCAGgtacgcgcacccgcggccaaacc	150
	S I A T L F G S	16
151	cggccggaaacctgacaaaacagcacagCACATCGGGCACTGCGCTGGGCC	200
	T S G T A L G P	24
201	CCGTGGAAATCACAGGACTGCACCTCAGTCACCGGGGTATCAATGCT	250
	R G N H S D C T S V D R G Y Q C F	41
251	TCCCTGAGCTCTCCATAAAATGGGTCTCTACGCGCCCTATTCTCCCTC	300
	P E L S H K W G L Y A P Y F S L	57
301	CAGGATGAATCTCGTTCTGGACGTCCCGATGACTGCCACATCAC	350
	Q D E S P F P L D V P D D C H I T	74
351	CTTGTGCAGGTGCTGGCCCGACATGGAGCGGGCTCCACCGATAGCA	400
	F V Q V L A R K G A R S P T D S K	91
401	AGACAAAAGCGTATGCCGGACTATTGCAGCCATCCAGAAGAATGCCACC	450
	T K A Y A A T I A A I Q K N A T	107
451	GGTTGCCGGCAAATACGCCCTCTGAAGTCGTACAATTACTCCATGGG	500
	A L P G K Y A F L K S Y N Y S M G	124
501	CTCCGAGAACCTGAACCCCTCGGGCGGAACCAACTGCAAGATCTGGCG	550
	S E N L N P F G R N Q L Q D L G A	141
551	CCCAGTTCTACCGTCGCTACGACACCCCTCACCCGGCACATCAACCCCTTC	600
	Q F Y R R Y D T L T R K I N P F	157
601	GTCCGGGCCGGATTCTCCCGGTCCACGAATCAGCCGAGAAGTCGT	650
	V R A A D S S R V H E S A E K F V	174

Figure 7/2

651	CGAGGGCTTCCAAAACGCCCGCCAAGGCCATCTCACGCCAACCCCTCACC E G F Q N A R Q G D P K A N P K Q	700 191
701	AGCCGTCGCCGGCGCGTGGATGTAGTCATCCCCGAAGGCACCCCTACAA P S P R V D V V I P E G T A Y N	750 207
751	AACACGCTCGAGCACAGCATCTGCACCGCTTCGAGGCCAGCACCGTCGG N T L E H S I C T A F E A S T V G	800 224
801	CGACGCCCGGGCAGACAACCTCACTGCCGTGTCGCCGGCGATGCCA D A A A D N F T A V F A P A I A K	850 241
851	AGCGTCTGGAGGCCGATCTGCCCGGGCGTCAGCTGTCCGCCAGCACGTG R L E A S L P G V Q L S A D D V	900 257
901	GTCAAATCTGATGCCCATGTCCTGGAGACCGCTCACCTGACCGACGA V N L M A M C P F E T V S L T D D	950 274
951	<u>CGCGCACACGGCTGTGCCCGTUTGCCGACCTCTCACCGCCGCCAGTGGA</u> A H T L S P F C D L F T A A E W T	1000 291
1001	<u>CGCAGTACAACCTACCTGCTCTCGCTGGACAAGTACTACGGCTACGGCGC</u> Q Y N Y L L S L D K Y Y G Y G G	1050 307
1051	GGCAATCCGCTGGGCCCGTGCAGGGCGTGGCTGGCGAACGAGCTGAT G N P L G P V Q G V G W A N E L I	1100 324
1101	CGCGCGGCTGACGGCTCCCCCGTCCACGACCACACCTGCCGTCAACACA A R L T R S P V K D K T C V N N T	1150 341
1151	CCCTCGACGCCAACCGGCCACCTTCCCGTGAACGCCACCCCTACCGC L D A N P A T F P L N A T L Y A	1200 357
1201	GACTTTGGCACCGACAGTAACCTGGTGTGATCTCTGGCGCTGGCT D F S K D S N L V S I F W A L G L	1250 374

Figure 7/3

1251 GTCCAACGGCACCAGCCTGTCGCAGACCACCGTGGACGATATCACCC 1300  
 Y N G T K P L S Q T T V E D I T R 391  
 \*  
 1301 GCACCGACCGCTACCGCCGCCCTCGACGTTCCCGATTCCCCCCCCCCCC 1350  
 T D G Y A A A W T V P F A A R A 407  
 1351 TACATCGAGATGATGCAGAGTGTCCCGCCGAGAACGAGCCGCTGGTGCCG 1400  
 Y I E M M Q C R A E K Q P L V R V 424  
 1401 GCTGGTCAACGACCGTGTCATCCGCTGCACGGCTGGCGGTGGATATC 1450  
 L V N D R V M P L H G C A V D N L 441  
 1451 TGGGCACGTGTAAACGGGACGACTTGTGGAGGGACTGAGCTTGCGCGG 1500  
 G R C K R D D F V E G L S F A R 457  
 1501 GCACGGACGGAACTGGCCGAGTGTTTCTGATGTACATGCTGTAGTAGCT 1550  
 A G G N W A S C F \* 466  
 1551 TTGAGTCCTGAGGTACC 1567

Figure 8/1

HEADER Phosphomonoesterase 1  
 COMPND Phytase (E.C.3.1.3.8) 2  
 SOURCE (Aspergillus ficuum) 3  
 1DIK 1  
 1DIK 2  
 1DIK 3  
 1DIK 4  
 1DIK 5  
 1DIK 6  
 1DIK 7  
 1DIK 8  
 1DIK 9  
 1DIK 10  
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 1DIK 99

REMARK 2 RESOLUTION. 2.5 ANGSTROMS. 1  
 REMARK 3 1  
 REMARK 3 REFINEMENT. 2  
 REMARK 3 PROGRAM X-PLOR 3  
 REMARK 3 AUTHORS BRUENGER, A.T. 4  
 REMARK 3 R VALUE 0.155 5  
 REMARK 3 FREE R VALUE 0.211 6  
 REMARK 3 RMSD BOND DISTANCES 0.009 ANGSTROMS 7  
 REMARK 3 RMSD BOND ANGLES 1.5 DEGREES 8  
 REMARK 3 NUMBER OF REFLECTIONS 17206 9  
 REMARK 3 RESOLUTION RANGE 20.0 - 2.5 ANGSTROMS 10  
 REMARK 3 DATA CUTOFF 0. SIGMA(F) 11  
 REMARK 3 NUMBER OF PROTEIN ATOMS 3369 12  
 REMARK 3 NUMBER OF SOLVENT ATOMS 115 13  
 REMARK 3 NUMBER OF SULFATE ATOMS 5 14  
 REMARK 3 CONVENTIONAL RESTRAINED POSITIONAL AND TEMPERATURE FACTOR 15  
 REMARK 3 REFINEMENT. 16  
 REMARK 3 THE STEREOCHEMICAL PARAMETERS FROM ENGH & HUBER WERE USED. 17  
 REMARK 4 18  
 REMARK 5 19  
 REMARK 5 THE ASYMMETRIC UNIT OF THE CRYSTAL CONTAINS OF ONE 20  
 REMARK 5 DEGLYCOSYLATED PROTEIN MONOMER. 21  
 REMARK 6 22  
 REMARK 6 THE AMINO ACIDS 249 - 252 ARE COMPLETELY DISORDERED. 23  
 REMARK 6 THE FOLLOWING AMINO ACID SIDE CHAINS ARE DISORDERED: 24  
 REMARK 6 GLU 43, LYS 70, GLU 77, GLN 81, LYS 94, GLN 392, GLN 395. 25  
 REMARK 6 ARG 428 26  
 REMARK 6 THE ELECTRON DENSITY OF THE SULFATE IS NOT WELL DEFINED. 27  
 SEQRES 1 434 SER CYS ASP THR VAL ASP GLN GLY TYR GLN CYS PHE SER 28  
 SEQRES 2 434 GLU THR SER HIS LEU TRP GLY GLN TYR ALA PRO PHE PHE 29  
 SEQRES 3 434 SER LEU ALA ASN GLU SER VAL ILE SER PRO GLU VAL PRO 30  
 SEQRES 4 434 ALA GLY CYS ARG VAL THR PHE ALA GLN VAL LEU SER ARG 31  
 SEQRES 5 434 HIS GLY ALA ARG TYR PRO THR ASP SER LYS GLY LYS LYS 32  
 SEQRES 6 434 TYR SER ALA LEU ILE GLU GLU ILE GLN GLN ASN ALA THR 33  
 SEQRES 7 434 THR PHE ASP GLY LYS TYR ALA PHE LEU LYS THR TYR ASN 34  
 SEQRES 8 434 TYR SER LEU GLY ALA ASP ASP LEU THR PRO PHE GLY GLU 35  
 SEQRES 9 434 GLN GLU LEU VAL ASN SER GLY ILE LYS PHE TYR GLN ARG 36  
 SEQRES 10 434 TYR GLU SER LEU THR ARG ASN ILE VAL PRO PHE ILE ARG 37  
 SEQRES 11 434 SER SER GLY SER SER ARG VAL ILE ALA SER GLY LYS LYS 38  
 SEQRES 12 434 PHE ILE GLU GLY PHE GLN SER THR LYS LEU LYS ASP PRO 39  
 SEQRES 13 434 ARG ALA GLN PRO GLY GLN SER SER PRO LYS ILE ASP VAL 40  
 SEQRES 14 434 VAL ILE SER GLU ALA SER SER ASN ASN THR LEU ASP 41  
 SEQRES 15 434 PRO GLY THR CYS THR VAL PHE GLU ASP SER GLU LEU ALA 42  
 SEQRES 16 434 ASP THR VAL GLU ALA ASN PHE THR ALA THR PHE VAL PRO 43  
 SEQRES 17 434 SER ILE ARG GLN ARG LEU GLU ASN ASP LEU SER GLY VAL 44  
 SEQRES 18 434 THR LEU THR ASP THR GLU VAL THR TYR LEU MET ASP MET 45  
 SEQRES 19 434 CYS SER PHE ASP THR ILE SER THR THR LYS LEU SER PRO 46  
 SEQRES 20 434 PHE CYS ASP LEU PHE THR HIS ASP GLU TRP ILE ASN TYR 47  
 SEQRES 21 434 ASP TYR LEU GLN SER LEU LYS LYS TYR TYR GLY HIS GLY 48  
 SEQRES 22 434 ALA GLY ASN PRO LEU GLY PRO THR GLN GLY VAL GLY TYR 49  
 SEQRES 23 434 ALA ASN GLU LEU ILE ALA ARG LEU THR HIS SER PRO VAL 50  
 SEQRES 24 434 HIS ASP ASP THR SER SER ASN HIS THR LEU ASP SER SER 51  
 SEQRES 25 434 PRO ALA THR PHE PRO LEU ASN SER THR LEU TYR ALA ASP 52  
 SEQRES 26 434 PHE SER HIS ASP ASN GLY ILE ILE SER ILE LEU PHE ALA 53  
 SEQRES 27 434 LEU GLY LEU TYR ASN GLY THR LYS PRO LEU SER THR THR 54  
 SEQRES 28 434 THR VAL GLU ASN ILE THR GLN THR ASP GLY PHE SER SER 55  
 SEQRES 29 434 ALA TRP THR VAL PRO PHE ALA SER ARG LEU TYR VAL GLU 56  
 SEQRES 30 434 MET MET GLN CYS GLN ALA GLU GLN GLU PRO LEU VAL ARG 57  
 SEQRES 31 434 VAL LEU VAL ASN ASP ARG VAL VAL PRO LEU HIS GLY CYS 58  
 SEQRES 32 434 PRO VAL ASP ALA LEU GLY ARG CYS THR ARG ASP SER PHE 59  
 SEQRES 33 434 VAL ARG GLY LEU SER PHE ALA ARG SER GLY GLY ASP TRP 60  
 SEQRES 34 434 ALA GLU CYS PHE ALA 61

HET SO4 201 5 6 6 1DIK 93  
 FORMUL 2 SO4 O4 S1 1DIK 94  
 FORMUL 3 HOH \*115(H2 O1) 1DIK 95  
 SSBOND 1 CYS 8 CYS 17 1DIK 96  
 SSBOND 2 CYS 48 CYS 391 1DIK 97  
 SSBOND 3 CYS 192 CYS 442 1DIK 98  
 SSBOND 4 CYS 241 CYS 259 1DIK 99  
 SSBOND 5 CYS 413 CYS 421 1DIK 100

CRYST1 92.250 92.250 100.890 90.00 90.00 120.00 P 3 2 1 6 1DIK 101  
 ATOM 1 N SER 7 -18.097 39.685 9.811 1.00 62.21 1DIK 102  
 ATOM 2 CA SER 7 -17.205 40.761 9.300 1.00 63.47 1DIK 103  
 ATOM 3 C SER 7 -16.157 41.230 10.307 1.00 63.25 1DIK 104  
 ATOM 4 O SER 7 -15.210 41.924 9.918 1.00 63.40 1DIK 105  
 ATOM 5 CB SER 7 -18.027 41.947 8.800 1.00 64.21 1DIK 106  
 ATOM 7 OG SER 7 -18.983 41.499 7.850 1.00 69.41 1DIK 107

Figure 8/2

ATOM	8	N	CYS	8	-16.314	40.885	11.590	1.00	60.09	1DIK 100
ATOM	9	CA	CYS	8	-15.278	41.262	12.561	1.00	57.19	1DIK 101
ATOM	10	C	CYS	8	-14.528	40.052	13.134	1.00	54.36	1DIK 102
ATOM	11	O	CYS	8	-13.593	40.225	13.913	1.00	54.16	1DIK 103
ATOM	12	CB	CYS	8	-15.738	42.278	13.657	1.00	55.87	1DIK 104
ATOM	13	SG	CYS	8	-17.414	42.211	14.391	1.00	47.31	1DIK 105
ATOM	14	N	ASP	9	-14.945	38.838	12.748	1.00	49.46	1DIK 106
ATOM	15	CA	ASP	9	-14.217	37.609	13.109	1.00	44.53	1DIK 107
ATOM	16	C	ASP	9	-13.647	37.121	11.763	1.00	43.95	1DIK 108
ATOM	17	O	ASP	9	-14.380	36.543	10.956	1.00	45.30	1DIK 109
ATOM	18	CB	ASP	9	-15.112	36.512	13.687	1.00	36.86	1DIK 110
ATOM	19	CG	ASP	9	-14.324	35.205	13.981	1.00	43.08	1DIK 111
ATOM	20	OD1	ASP	9	-13.169	35.246	14.466	1.00	36.37	1DIK 112
ATOM	21	OD2	ASP	9	-14.860	34.107	13.725	1.00	53.20	1DIK 113
ATOM	22	N	THR	10	-12.360	37.357	11.515	1.00	39.20	1DIK 114
ATOM	23	CA	THR	10	-11.744	36.961	10.248	1.00	34.97	1DIK 115
ATOM	24	C	THR	10	-10.770	35.792	10.388	1.00	35.15	1DIK 116
ATOM	25	O	THR	10	-10.407	35.410	11.502	1.00	32.93	1DIK 117
ATOM	26	CB	THR	10	-10.988	38.148	9.605	1.00	32.39	1DIK 118
ATOM	27	OG1	THR	10	-9.967	38.612	10.500	1.00	36.02	1DIK 119
ATOM	28	CG2	THR	10	-11.937	39.286	9.319	1.00	24.30	1DIK 120
ATOM	29	N	VAL	11	-10.352	35.228	9.256	1.00	35.93	1DIK 121
ATOM	30	CA	VAL	11	-9.398	34.123	9.261	1.00	35.37	1DIK 122
ATOM	31	C	VAL	11	-8.050	34.591	9.798	1.00	36.90	1DIK 123
ATOM	32	O	VAL	11	-7.442	33.912	10.623	1.00	38.05	1DIK 124
ATOM	33	CB	VAL	11	-9.196	33.528	7.840	1.00	36.34	1DIK 125
ATOM	34	CG1	VAL	11	-7.982	32.584	7.806	1.00	29.66	1DIK 126
ATOM	35	CG2	VAL	11	-10.440	32.772	7.429	1.00	36.32	1DIK 127
ATOM	36	N	ASP	12	-7.585	35.749	9.334	1.00	36.93	1DIK 128
ATOM	37	CA	ASP	12	-6.298	36.277	9.774	1.00	35.36	1DIK 129
ATOM	38	C	ASP	12	-6.298	37.009	11.094	1.00	32.61	1DIK 130
ATOM	39	O	ASP	12	-5.449	36.757	11.930	1.00	31.31	1DIK 131
ATOM	40	CB	ASP	12	-5.698	37.195	8.712	1.00	44.11	1DIK 132
ATOM	41	CG	ASP	12	-4.974	36.428	7.629	1.00	34.17	1DIK 133
ATOM	42	OD1	ASP	12	-3.831	35.998	7.891	1.00	59.05	1DIK 134
ATOM	43	OD2	ASP	12	-5.540	36.252	6.523	1.00	57.68	1DIK 135
ATOM	44	N	GLN	13	-7.241	37.918	11.294	1.00	31.17	1DIK 136
ATOM	45	CA	GLN	13	-7.251	38.684	12.530	1.00	31.70	1DIK 137
ATOM	46	C	GLN	13	-7.944	38.049	13.741	1.00	30.12	1DIK 138
ATOM	47	O	GLN	13	-7.706	38.450	14.879	1.00	26.40	1DIK 139
ATOM	48	CB	GLN	13	-7.804	40.090	12.265	1.00	38.39	1DIK 140
ATOM	49	CG	GLN	13	-6.865	40.982	11.450	1.00	44.04	1DIK 141
ATOM	50	CD	GLN	13	-5.467	41.085	12.071	1.00	53.25	1DIK 142
ATOM	51	OE1	GLN	13	-5.251	41.806	13.055	1.00	56.16	1DIK 143
ATOM	52	NE2	GLN	13	-4.510	40.357	11.497	1.00	59.15	1DIK 144
ATOM	53	N	GLY	14	-8.792	37.057	13.520	1.00	26.13	1DIK 145
ATOM	54	CA	GLY	14	-9.476	36.460	14.648	1.00	23.53	1DIK 146
ATOM	55	C	GLY	14	-10.684	37.301	15.001	1.00	23.28	1DIK 147
ATOM	56	O	GLY	14	-11.198	38.031	14.162	1.00	21.73	1DIK 148
ATOM	57	N	TYR	15	-11.137	37.211	16.241	1.00	26.17	1DIK 149
ATOM	58	CA	TYR	15	-12.312	37.944	16.682	1.00	27.82	1DIK 150
ATOM	59	C	TYR	15	-12.033	39.383	17.139	1.00	29.70	1DIK 151
ATOM	60	O	TYR	15	-11.437	39.617	18.200	1.00	30.97	1DIK 152
ATOM	61	CB	TYR	15	-12.986	37.154	17.786	1.00	27.03	1DIK 153
ATOM	62	CG	TYR	15	-14.380	37.607	18.120	1.00	31.13	1DIK 154
ATOM	63	CD1	TYR	15	-15.471	37.146	17.386	1.00	30.29	1DIK 155
ATOM	64	CD2	TYR	15	-14.620	38.456	19.203	1.00	29.69	1DIK 156
ATOM	65	CE1	TYR	15	-16.767	37.512	17.721	1.00	33.21	1DIK 157
ATOM	66	CE2	TYR	15	-15.912	38.829	19.549	1.00	30.40	1DIK 158
ATOM	67	CZ	TYR	15	-16.982	38.355	18.808	1.00	34.78	1DIK 159
ATOM	68	OH	TYR	15	-18.266	38.709	19.151	1.00	36.84	1DIK 160
ATOM	69	N	GLN	16	-12.482	40.336	16.327	1.00	28.71	1DIK 161
ATOM	70	CA	GLN	16	-12.293	41.760	16.583	1.00	31.69	1DIK 162
ATOM	71	C	GLN	16	-13.566	42.534	16.957	1.00	30.38	1DIK 163
ATOM	72	O	GLN	16	-13.543	43.754	17.038	1.00	35.26	1DIK 164
ATOM	73	CB	GLN	16	-11.616	42.419	15.367	1.00	32.17	1DIK 165
ATOM	74	CG	GLN	16	-10.250	41.819	14.974	1.00	34.26	1DIK 166
ATOM	75	CD	GLN	16	-9.212	41.894	16.098	1.00	40.25	1DIK 167
ATOM	76	OE1	GLN	16	-9.300	42.740	16.991	1.00	44.10	1DIK 168
ATOM	77	NE2	GLN	16	-8.227	41.003	16.060	1.00	37.91	1DIK 169
ATOM	78	N	CYS	17	-14.673	41.836	17.182	1.00	32.53	1DIK 170
ATOM	79	CA	CYS	17	-15.934	42.483	17.563	1.00	34.82	1DIK 171
ATOM	80	C	CYS	17	-15.880	42.811	19.062	1.00	32.69	1DIK 172
ATOM	81	O	CYS	17	-15.355	42.015	19.843	1.00	34.59	1DIK 173
ATOM	82	CB	C							

Figure 8/3

ATOM	93	CE2	PHE	18	-20.180	41.691	19.729	1.00	19.40	1DIK 185
ATOM	94	CZ	PHE	18	-21.100	42.695	19.451	1.00	21.61	1DIK 186
ATOM	95	N	SER	19	-13.997	44.422	20.912	1.00	29.30	1DIK 187
ATOM	96	CA	SER	19	-12.648	44.228	21.461	1.00	30.72	1DIK 188
ATOM	97	C	SER	19	-12.361	44.754	22.857	1.00	31.50	1DIK 189
ATOM	98	O	SER	19	-11.619	44.128	23.617	1.00	32.76	1DIK 190
ATOM	99	CB	SER	19	-11.603	44.799	20.500	1.00	28.75	1DIK 191
ATOM	100	OG	SER	19	-11.757	46.201	20.381	1.00	33.48	1DIK 192
ATOM	101	N	GLU	20	-12.939	45.899	23.192	1.00	31.46	1DIK 193
ATOM	102	CA	GLU	20	-12.715	46.498	24.497	1.00	34.60	1DIK 194
ATOM	103	C	GLU	20	-13.323	45.653	25.626	1.00	33.63	1DIK 195
ATOM	104	O	GLU	20	-12.963	45.832	26.786	1.00	35.88	1DIK 196
ATOM	105	CB	GLU	20	-13.214	47.961	24.522	1.00	36.86	1DIK 197
ATOM	106	CG	GLU	20	-14.736	48.175	24.598	1.00	47.02	1DIK 198
ATOM	107	CD	GLU	20	-15.534	47.635	23.389	1.00	56.13	1DIK 199
ATOM	108	OE1	GLU	20	-15.103	47.815	22.218	1.00	56.48	1DIK 200
ATOM	109	OE2	GLU	20	-16.615	47.025	23.618	1.00	58.06	1DIK 201
ATOM	110	N	THR	21	-14.234	44.736	25.288	1.00	30.34	1DIK 202
ATOM	111	CA	THR	21	-14.861	43.832	26.267	1.00	27.14	1DIK 203
ATOM	112	C	THR	21	-14.525	42.355	25.983	1.00	26.26	1DIK 204
ATOM	113	O	THR	21	-14.048	41.641	26.868	1.00	24.39	1DIK 205
ATOM	114	CB	THR	21	-16.405	43.965	26.272	1.00	26.34	1DIK 206
ATOM	115	OG1	THR	21	-16.758	45.337	26.448	1.00	32.63	1DIK 207
ATOM	116	CG2	THR	21	-17.026	43.137	27.395	1.00	15.06	1DIK 208
ATOM	117	N	SER	22	-14.763	41.903	24.750	1.00	24.89	1DIK 209
ATOM	118	CA	SER	22	-14.533	40.506	24.377	1.00	21.13	1DIK 210
ATOM	119	C	SER	22	-13.105	40.015	24.621	1.00	20.85	1DIK 211
ATOM	120	O	SER	22	-12.896	38.837	24.919	1.00	19.87	1DIK 212
ATOM	121	CB	SER	22	-14.924	40.282	22.918	1.00	16.59	1DIK 213
ATOM	122	OG	SER	22	-14.015	40.939	22.044	1.00	23.72	1DIK 214
ATOM	123	N	HIS	23	-12.126	40.911	24.497	1.00	20.46	1DIK 215
ATOM	124	CA	HIS	23	-10.726	40.555	24.708	1.00	20.05	1DIK 216
ATOM	125	C	HIS	23	-10.329	40.455	26.183	1.00	24.47	1DIK 217
ATOM	126	O	HIS	23	-9.196	40.084	26.496	1.00	25.61	1DIK 218
ATOM	127	CB	HIS	23	-9.800	41.536	23.982	1.00	17.77	1DIK 219
ATOM	128	CG	HIS	23	-9.861	41.426	22.484	1.00	24.57	1DIK 220
ATOM	129	ND1	HIS	23	-8.936	42.020	21.651	1.00	20.40	1DIK 221
ATOM	130	CD2	HIS	23	-10.746	40.795	21.670	1.00	23.97	1DIK 222
ATOM	131	CE1	HIS	23	-9.247	41.764	20.392	1.00	20.67	1DIK 223
ATOM	132	NE2	HIS	23	-10.340	41.022	20.376	1.00	23.06	1DIK 224
ATOM	133	N	LEU	24	-11.263	40.776	27.081	1.00	25.15	1DIK 225
ATOM	134	CA	LEU	24	-11.025	40.716	28.524	1.00	24.99	1DIK 226
ATOM	135	C	LEU	24	-11.739	39.538	29.210	1.00	27.65	1DIK 227
ATOM	136	O	LEU	24	-11.984	39.575	30.421	1.00	25.05	1DIK 228
ATOM	137	CB	LEU	24	-11.455	42.034	29.176	1.00	22.74	1DIK 229
ATOM	138	CG	LEU	24	-10.626	43.258	28.774	1.00	22.62	1DIK 230
ATOM	139	CD1	LEU	24	-11.264	44.509	29.324	1.00	23.25	1DIK 231
ATOM	140	CD2	LEU	24	-9.211	43.126	29.281	1.00	15.42	1DIK 232
ATOM	141	N	TRP	25	-12.062	38.496	28.437	1.00	26.64	1DIK 233
ATOM	142	CA	TRP	25	-12.744	37.317	28.961	1.00	21.87	1DIK 234
ATOM	143	C	TRP	25	-11.811	36.148	29.357	1.00	22.59	1DIK 235
ATOM	144	O	TRP	25	-12.283	35.040	29.625	1.00	22.32	1DIK 236
ATOM	145	CB	TRP	25	-13.804	36.845	27.951	1.00	22.87	1DIK 237
ATOM	146	CG	TRP	25	-14.977	37.813	27.754	1.00	25.99	1DIK 238
ATOM	147	CD1	TRP	25	-15.376	38.805	28.615	1.00	22.03	1DIK 239
ATOM	148	CD2	TRP	25	-15.880	37.877	26.626	1.00	23.51	1DIK 240
ATOM	149	NE1	TRP	25	-16.459	39.475	28.094	1.00	22.08	1DIK 241
ATOM	150	CE2	TRP	25	-16.792	38.931	26.877	1.00	24.34	1DIK 242
ATOM	151	CE3	TRP	25	-16.004	37.150	25.425	1.00	25.98	1DIK 243
ATOM	152	CZ2	TRP	25	-17.821	39.280	25.973	1.00	20.60	1DIK 244
ATOM	153	CZ3	TRP	25	-17.034	37.500	24.517	1.00	21.02	1DIK 245
ATOM	154	CH2	TRP	25	-17.923	38.555	24.804	1.00	20.24	1DIK 246
ATOM	155	N	GLY	26	-10.499	36.384	29.403	1.00	20.85	1DIK 247
ATOM	156	CA	GLY	26	-9.566	35.322	29.757	1.00	21.54	1DIK 248
ATOM	157	C	GLY	26	-9.676	34.138	28.806	1.00	21.52	1DIK 249
ATOM	158	O	GLY	26	-9.642	34.319	27.590	1.00	19.25	1DIK 250
ATOM	159	N	GLN	27	-9.819	32.927	29.346	1.00	23.90	1DIK 251
ATOM	160	CA	GLN	27	-9.946	31.740	28.503	1.00	24.89	1DIK 252
ATOM	161	C	GLN	27	-11.340	31.566	27.902	1.00	24.51	1DIK 253
ATOM	162	O	GLN	27	-11.600	30.573	27.226	1.00	25.98	1DIK 254
ATOM	163	CB	GLN	27	-9.535	30.455	29.245	1.00	23.84	1DIK 255
ATOM	164	CG	GLN	27	-10.472	29.995	30.323	1.00	21.01	1DIK 256
ATOM	165	CD	GLN	27	-10.344	30.823	31.573	1.00	27.35	1DIK 25

Figure 8/4

ATOM	178	CZ	TYR	28	-15.005	29.895	31.793	1.00	29.76	1DIK 270
ATOM	179	OH	TYR	28	-15.113	28.997	32.827	1.00	35.18	1DIK 271
ATOM	180	N	ALA	29	-12.480	34.061	26.111	1.00	21.55	1DIK 272
ATOM	181	CA	ALA	29	-12.340	35.025	25.029	1.00	21.69	1DIK 273
ATOM	182	C	ALA	29	-12.102	34.251	23.725	1.00	22.47	1DIK 274
ATOM	183	O	ALA	29	-11.401	33.233	23.720	1.00	22.07	1DIK 275
ATOM	184	CB	ALA	29	-11.139	35.944	25.305	1.00	12.96	1DIK 276
ATOM	185	N	PRO	30	-12.709	34.697	22.612	1.00	24.01	1DIK 277
ATOM	186	CA	PRO	30	-12.509	34.027	21.319	1.00	20.94	1DIK 278
ATOM	187	C	PRO	30	-11.099	34.409	20.841	1.00	19.17	1DIK 279
ATOM	188	O	PRO	30	-10.608	35.498	21.155	1.00	18.52	1DIK 280
ATOM	189	CB	PRO	30	-13.568	34.671	20.414	1.00	20.61	1DIK 281
ATOM	190	CG	PRO	30	-14.540	35.324	21.362	1.00	24.76	1DIK 282
ATOM	191	CD	PRO	30	-13.651	35.819	22.480	1.00	25.47	1DIK 283
ATOM	192	N	PHE	31	-10.438	33.533	20.093	1.00	20.80	1DIK 284
ATOM	193	CA	PHE	31	-9.102	33.861	19.596	1.00	19.54	1DIK 285
ATOM	194	C	PHE	31	-9.077	35.195	18.814	1.00	20.93	1DIK 286
ATOM	195	O	PHE	31	-9.957	35.482	17.984	1.00	20.23	1DIK 287
ATOM	196	CB	PHE	31	-8.552	32.723	18.692	1.00	17.50	1DIK 288
ATOM	197	CG	PHE	31	-7.448	33.165	17.750	1.00	19.27	1DIK 289
ATOM	198	CD1	PHE	31	-6.119	33.222	18.181	1.00	21.10	1DIK 290
ATOM	199	CD2	PHE	31	-7.747	33.579	16.435	1.00	18.79	1DIK 291
ATOM	200	CE1	PHE	31	-5.105	33.692	17.318	1.00	21.44	1DIK 292
ATOM	201	CE2	PHE	31	-6.741	34.050	15.564	1.00	14.12	1DIK 293
ATOM	202	CZ	PHE	31	-5.426	34.108	16.005	1.00	17.15	1DIK 294
ATOM	203	N	PHE	32	-8.067	36.005	19.097	1.00	18.45	1DIK 295
ATOM	204	CA	PHE	32	-7.844	37.244	18.368	1.00	20.59	1DIK 296
ATOM	205	C	PHE	32	-6.324	37.260	18.121	1.00	20.82	1DIK 297
ATOM	206	O	PHE	32	-5.536	36.921	19.002	1.00	23.47	1DIK 298
ATOM	207	CB	PHE	32	-8.350	38.480	19.131	1.00	19.12	1DIK 299
ATOM	208	CG	PHE	32	-7.872	38.573	20.560	1.00	23.83	1DIK 300
ATOM	209	CD1	PHE	32	-8.508	37.845	21.577	1.00	20.95	1DIK 301
ATOM	210	CD2	PHE	32	-6.806	39.406	20.896	1.00	19.92	1DIK 302
ATOM	211	CE1	PHE	32	-8.095	37.946	22.896	1.00	20.93	1DIK 303
ATOM	212	CE2	PHE	32	-6.382	39.517	22.219	1.00	22.76	1DIK 304
ATOM	213	CZ	PHE	32	-7.032	38.783	23.226	1.00	23.83	1DIK 305
ATOM	214	N	SER	33	-5.914	37.623	16.915	1.00	20.87	1DIK 306
ATOM	215	CA	SER	33	-4.504	37.635	16.571	1.00	22.19	1DIK 307
ATOM	216	C	SER	33	-3.672	38.690	17.284	1.00	23.15	1DIK 308
ATOM	217	O	SER	33	-4.041	39.870	17.320	1.00	23.04	1DIK 309
ATOM	218	CB	SER	33	-4.329	37.796	15.060	1.00	22.81	1DIK 310
ATOM	219	OG	SER	33	-2.947	37.792	14.729	1.00	25.39	1DIK 311
ATOM	220	N	LEU	34	-2.544	38.263	17.846	1.00	23.77	1DIK 312
ATOM	221	CA	LEU	34	-1.638	39.188	18.523	1.00	25.51	1DIK 313
ATOM	222	C	LEU	34	-0.492	39.605	17.606	1.00	26.78	1DIK 314
ATOM	223	O	LEU	34	0.501	40.148	18.084	1.00	26.99	1DIK 315
ATOM	224	CB	LEU	34	-1.063	38.572	19.796	1.00	23.17	1DIK 316
ATOM	225	CG	LEU	34	-2.087	38.252	20.887	1.00	25.71	1DIK 317
ATOM	226	CD1	LEU	34	-1.395	37.465	21.984	1.00	23.09	1DIK 318
ATOM	227	CD2	LEU	34	-2.712	39.528	21.427	1.00	19.78	1DIK 319
ATOM	228	N	ALA	35	-0.639	39.365	16.301	1.00	27.00	1DIK 320
ATOM	229	CA	ALA	35	0.390	39.711	15.319	1.00	31.06	1DIK 321
ATOM	230	C	ALA	35	0.835	41.166	15.428	1.00	35.74	1DIK 322
ATOM	231	O	ALA	35	2.025	41.455	15.344	1.00	39.04	1DIK 323
ATOM	232	CB	ALA	35	-0.103	39.434	13.915	1.00	24.83	1DIK 324
ATOM	233	N	ASN	36	-0.118	42.075	15.623	1.00	39.86	1DIK 325
ATOM	234	CA	ASN	36	0.181	43.506	15.737	1.00	41.12	1DIK 326
ATOM	235	C	ASN	36	0.815	43.897	17.057	1.00	40.64	1DIK 327
ATOM	236	O	ASN	36	1.319	45.010	17.188	1.00	42.67	1DIK 328
ATOM	237	CB	ASN	36	-1.084	44.349	15.538	1.00	43.24	1DIK 329
ATOM	238	CG	ASN	36	-1.671	44.193	14.156	1.00	49.12	1DIK 330
ATOM	239	OD1	ASN	36	-0.945	44.021	13.172	1.00	50.49	1DIK 331
ATOM	240	ND2	ASN	36	-2.995	44.246	14.066	1.00	56.59	1DIK 332
ATOM	241	N	GLU	37	0.784	43.000	18.039	1.00	39.04	1DIK 333
ATOM	242	CA	GLU	37	1.380	43.287	19.347	1.00	39.87	1DIK 334
ATOM	243	C	GLU	37	2.788	42.722	19.440	1.00	37.45	1DIK 335
ATOM	244	O	GLU	37	3.506	42.963	20.411	1.00	38.65	1DIK 336
ATOM	245	CB	GLU	37	0.530	42.693	20.478	1.00	43.47	1DIK 337
ATOM	246	CG	GLU	37	-0.796	43.401	20.721	1.00	47.80	1DIK 338
ATOM	247	CD	GLU	37	-0.616	44.863	21.087	1.00	51.75	1DIK 339
ATOM	248	OE1	GLU	37	0.084	45.166	22.088	1.00	51.94	1DIK 340
ATOM	249	OE2	GLU	37	-1.183	45.710	20.357	1.00	55.20	1DIK 341
ATOM	250	N	SER	38	3.174	41.961	18.425	1.00	35.62	1DIK 342
ATOM	251	CA	SER	38	4.482	41.340	18.389</			

Figure 8/5

ATOM	263	N	ILE	40	8.645	41.434	17.239	1.00	32.27	1DIK 355
ATOM	264	CA	ILE	40	9.323	40.766	16.127	1.00	29.21	1DIK 356
ATOM	265	C	ILE	40	8.262	40.386	15.083	1.00	28.46	1DIK 357
ATOM	266	O	ILE	40	7.195	39.885	15.440	1.00	26.34	1DIK 358
ATOM	267	CB	ILE	40	10.059	39.494	16.624	1.00	29.64	1DIK 359
ATOM	268	CG1	ILE	40	11.147	39.900	17.631	1.00	30.03	1DIK 360
ATOM	269	CG2	ILE	40	10.633	38.721	15.436	1.00	26.81	1DIK 361
ATOM	270	CD1	ILE	40	11.771	38.777	18.437	1.00	26.07	1DIK 362
ATOM	271	N	SER	41	8.548	40.626	13.806	1.00	29.09	1DIK 363
ATOM	272	CA	SER	41	7.594	40.302	12.737	1.00	30.76	1DIK 364
ATOM	273	C	SER	41	7.310	38.798	12.646	1.00	29.37	1DIK 365
ATOM	274	O	SER	41	8.234	37.990	12.552	1.00	28.10	1DIK 366
ATOM	275	CB	SER	41	8.113	40.802	11.386	1.00	29.99	1DIK 367
ATOM	276	OG	SER	41	7.148	40.555	10.379	1.00	32.70	1DIK 368
ATOM	277	N	PRO	42	6.021	38.410	12.664	1.00	31.46	1DIK 369
ATOM	278	CA	PRO	42	5.577	37.009	12.592	1.00	30.99	1DIK 370
ATOM	279	C	PRO	42	5.915	36.287	11.285	1.00	31.80	1DIK 371
ATOM	280	O	PRO	42	5.950	35.062	11.241	1.00	34.31	1DIK 372
ATOM	281	CB	PRO	42	4.056	37.109	12.791	1.00	28.85	1DIK 373
ATOM	282	CG	PRO	42	3.832	38.432	13.454	1.00	32.81	1DIK 374
ATOM	283	CD	PRO	42	4.863	39.312	12.766	1.00	31.32	1DIK 375
ATOM	284	N	GLU	43	6.160	37.047	10.226	1.00	34.83	1DIK 376
ATOM	285	CA	GLU	43	6.467	36.483	8.917	1.00	36.61	1DIK 377
ATOM	286	C	GLU	43	7.765	35.703	8.835	1.00	35.76	1DIK 378
ATOM	287	O	GLU	43	8.757	36.046	9.480	1.00	37.48	1DIK 379
ATOM	288	CB	GLU	43	6.516	37.586	7.867	1.00	45.46	1DIK 380
ATOM	289	CG	GLU	43	5.236	38.394	7.734	1.00	61.52	1DIK 381
ATOM	290	CD	GLU	43	5.488	39.889	7.891	1.00	71.53	1DIK 382
ATOM	291	OE1	GLU	43	6.553	40.371	7.420	1.00	76.20	1DIK 383
ATOM	292	OE2	GLU	43	4.624	40.581	8.487	1.00	75.49	1DIK 384
ATOM	293	N	VAL	44	7.739	34.654	8.020	1.00	35.15	1DIK 385
ATOM	294	CA	VAL	44	8.900	33.806	7.785	1.00	34.87	1DIK 386
ATOM	295	C	VAL	44	9.900	34.708	7.060	1.00	36.04	1DIK 387
ATOM	296	O	VAL	44	9.570	35.289	6.031	1.00	37.59	1DIK 388
ATOM	297	CB	VAL	44	8.529	32.582	6.883	1.00	33.01	1DIK 389
ATOM	298	CG1	VAL	44	9.757	31.698	6.657	1.00	28.63	1DIK 390
ATOM	299	CG2	VAL	44	7.398	31.773	7.522	1.00	26.10	1DIK 391
ATOM	300	N	PRO	45	11.131	34.837	7.590	1.00	38.73	1DIK 392
ATOM	301	CA	PRO	45	12.171	35.680	6.996	1.00	40.95	1DIK 393
ATOM	302	C	PRO	45	12.492	35.362	5.558	1.00	44.42	1DIK 394
ATOM	303	O	PRO	45	12.492	34.196	5.149	1.00	44.24	1DIK 395
ATOM	304	CB	PRO	45	13.382	35.431	7.893	1.00	39.65	1DIK 396
ATOM	305	CG	PRO	45	12.775	35.101	9.201	1.00	40.04	1DIK 397
ATOM	306	CD	PRO	45	11.645	34.183	8.806	1.00	40.88	1DIK 398
ATOM	307	N	ALA	46	12.769	36.418	4.798	1.00	48.71	1DIK 399
ATOM	308	CA	ALA	46	13.127	36.292	3.396	1.00	50.25	1DIK 400
ATOM	309	C	ALA	46	14.456	35.555	3.435	1.00	49.80	1DIK 401
ATOM	310	O	ALA	46	15.326	35.906	4.229	1.00	49.90	1DIK 402
ATOM	311	CB	ALA	46	13.304	37.577	2.777	1.00	50.74	1DIK 403
ATOM	312	N	GLY	47	14.613	34.533	2.600	1.00	47.13	1DIK 404
ATOM	313	CA	GLY	47	15.862	33.789	2.596	1.00	41.93	1DIK 405
ATOM	314	C	GLY	47	15.863	32.579	3.520	1.00	39.94	1DIK 406
ATOM	315	O	GLY	47	16.893	31.906	3.681	1.00	36.72	1DIK 407
ATOM	316	N	CYS	48	14.720	32.300	4.141	1.00	36.56	1DIK 408
ATOM	317	CA	CYS	48	14.609	31.139	5.012	1.00	34.94	1DIK 409
ATOM	318	C	CYS	48	13.549	30.237	4.434	1.00	34.24	1DIK 410
ATOM	319	O	CYS	48	12.669	30.684	3.693	1.00	33.85	1DIK 411
ATOM	320	CB	CYS	48	14.232	31.528	6.435	1.00	29.09	1DIK 412
ATOM	321	SG	CYS	48	15.506	32.511	7.263	1.00	30.08	1DIK 413
ATOM	322	N	ARG	49	13.643	28.962	4.775	1.00	32.71	1DIK 414
ATOM	323	CA	ARG	49	12.707	27.965	4.293	1.00	31.47	1DIK 415
ATOM	324	C	ARG	49	12.307	27.093	5.496	1.00	29.98	1DIK 416
ATOM	325	O	ARG	49	13.181	26.547	6.196	1.00	24.89	1DIK 417
ATOM	326	CB	ARG	49	13.424	27.153	3.219	1.00	34.59	1DIK 418
ATOM	327	CG	ARG	49	12.615	26.104	2.516	1.00	45.38	1DIK 419
ATOM	328	CD	ARG	49	13.520	25.363	1.547	1.00	50.77	1DIK 420
ATOM	329	NE	ARG	49	14.760	24.899	2.185	1.00	53.82	1DIK 421
ATOM	330	CZ	ARG	49	15.024	23.626	2.479	1.00	54.48	1DIK 422
ATOM	331	NH1	ARG	49	14.132	22.680	2.199	1.00	54.38	1DIK 423
ATOM	332	NH2	ARG	49	16.178	23.297	3.054	1.00	53.78	1DIK 424
ATOM	333	N	VAL	50	11.001	26.975	5.747	1.00	26.52	1DIK 425
ATOM	334	CA	VAL	50	10.510	26.167	6.865	1.00	23.44	1DIK 426
ATOM	335	C	VAL	50	10.718	24.689	6.555	1.00	22.87	1DIK 427
ATOM	336	O	VAL	50	10.383	24.223	5.472	1.00	24.36	1DIK 428
ATOM</td										

Figure 8/6

ATOM	348	CA	PHE	52	9.280	21.543	10.285	1.00	18.63	IDIK 440
ATOM	349	C	PHE	52	8.264	22.527	10.821	1.00	19.14	IDIK 441
ATOM	350	O	PHE	52	8.559	23.710	10.993	1.00	19.73	IDIK 442
ATOM	351	CB	PHE	52	10.211	21.081	11.425	1.00	17.98	IDIK 443
ATOM	352	CG	PHE	52	9.497	20.552	12.661	1.00	19.23	IDIK 444
ATOM	353	CD1	PHE	52	9.006	21.424	13.636	1.00	18.19	IDIK 445
ATOM	354	CD2	PHE	52	9.328	19.185	12.854	1.00	18.71	IDIK 446
ATOM	355	CE1	PHE	52	8.359	20.941	14.783	1.00	15.91	IDIK 447
ATOM	356	CE2	PHE	52	8.682	18.690	14.001	1.00	20.50	IDIK 448
ATOM	357	CZ	PHE	52	8.198	19.576	14.964	1.00	16.11	IDIK 449
ATOM	358	N	ALA	53	7.061	22.053	11.072	1.00	16.93	IDIK 450
ATOM	359	CA	ALA	53	6.045	22.910	11.647	1.00	19.01	IDIK 451
ATOM	360	C	ALA	53	5.112	22.048	12.468	1.00	19.84	IDIK 452
ATOM	361	O	ALA	53	4.647	21.002	12.011	1.00	21.85	IDIK 453
ATOM	362	CB	ALA	53	5.265	23.658	10.563	1.00	17.27	IDIK 454
ATOM	363	N	GLN	54	4.866	22.479	13.696	1.00	19.97	IDIK 455
ATOM	364	CA	GLN	54	3.924	21.801	14.570	1.00	16.77	IDIK 456
ATOM	365	C	GLN	54	2.963	22.820	15.172	1.00	13.22	IDIK 457
ATOM	366	O	GLN	54	3.370	23.901	15.592	1.00	15.19	IDIK 458
ATOM	367	CB	GLN	54	4.619	21.072	15.711	1.00	18.35	IDIK 459
ATOM	368	CG	GLN	54	3.595	20.527	16.697	1.00	24.84	IDIK 460
ATOM	369	CD	GLN	54	4.138	19.486	17.607	1.00	27.27	IDIK 461
ATOM	370	OE1	GLN	54	4.891	18.614	17.195	1.00	28.71	IDIK 462
ATOM	371	NE2	GLN	54	3.758	19.561	18.863	1.00	13.46	IDIK 463
ATOM	372	N	VAL	55	1.686	22.486	15.206	1.00	13.93	IDIK 464
ATOM	373	CA	VAL	55	0.721	23.372	15.822	1.00	14.13	IDIK 465
ATOM	374	C	VAL	55	0.094	22.604	16.990	1.00	14.94	IDIK 466
ATOM	375	O	VAL	55	-0.192	21.404	16.878	1.00	13.02	IDIK 467
ATOM	376	CB	VAL	55	-0.377	23.842	14.812	1.00	14.68	IDIK 468
ATOM	377	CG1	VAL	55	-1.062	22.645	14.155	1.00	8.55	IDIK 469
ATOM	378	CG2	VAL	55	-1.407	24.739	15.521	1.00	15.11	IDIK 470
ATOM	379	N	LEU	56	-0.076	23.292	18.111	1.00	11.84	IDIK 471
ATOM	380	CA	LEU	56	-0.719	22.731	19.278	1.00	11.96	IDIK 472
ATOM	381	C	LEU	56	-1.896	23.694	19.426	1.00	14.67	IDIK 473
ATOM	382	O	LEU	56	-1.721	24.903	19.647	1.00	13.79	IDIK 474
ATOM	383	CB	LEU	56	0.197	22.771	20.503	1.00	17.28	IDIK 475
ATOM	384	CG	LEU	56	-0.513	22.538	21.842	1.00	17.00	IDIK 476
ATOM	385	CD1	LEU	56	-1.065	21.122	21.949	1.00	13.43	IDIK 477
ATOM	386	CD2	LEU	56	0.472	22.817	22.938	1.00	17.28	IDIK 478
ATOM	387	N	SER	57	-3.095	23.162	19.277	1.00	16.89	IDIK 479
ATOM	388	CA	SER	57	-4.289	23.976	19.329	1.00	16.37	IDIK 480
ATOM	389	C	SER	57	-5.260	23.544	20.411	1.00	16.34	IDIK 481
ATOM	390	O	SER	57	-5.341	22.363	20.760	1.00	18.09	IDIK 482
ATOM	391	CB	SER	57	-4.984	23.906	17.960	1.00	15.08	IDIK 483
ATOM	392	OG	SER	57	-6.256	24.527	17.966	1.00	15.23	IDIK 484
ATOM	393	N	ARG	58	-5.986	24.514	20.946	1.00	14.89	IDIK 485
ATOM	394	CA	ARG	58	-7.015	24.257	21.934	1.00	16.34	IDIK 486
ATOM	395	C	ARG	58	-8.299	24.104	21.100	1.00	20.75	IDIK 487
ATOM	396	O	ARG	58	-8.352	24.546	19.940	1.00	20.55	IDIK 488
ATOM	397	CB	ARG	58	-7.159	25.457	22.874	1.00	14.15	IDIK 489
ATOM	398	CG	ARG	58	-8.315	25.320	23.835	1.00	13.80	IDIK 490
ATOM	399	CD	ARG	58	-8.411	26.468	24.791	1.00	15.28	IDIK 491
ATOM	400	NE	ARG	58	-9.551	26.299	25.692	1.00	16.96	IDIK 492
ATOM	401	CZ	ARG	58	-10.218	27.306	26.253	1.00	17.74	IDIK 493
ATOM	402	NH1	ARG	58	-9.863	28.564	26.021	1.00	19.32	IDIK 494
ATOM	403	NH2	ARG	58	-11.239	27.055	27.051	1.00	14.92	IDIK 495
ATOM	404	N	HIS	59	-9.326	23.478	21.673	1.00	22.89	IDIK 496
ATOM	405	CA	HIS	59	-10.620	23.324	20.993	1.00	21.80	IDIK 497
ATOM	406	C	HIS	59	-11.286	24.703	20.795	1.00	21.30	IDIK 498
ATOM	407	O	HIS	59	-10.860	25.693	21.403	1.00	20.60	IDIK 499
ATOM	408	CB	HIS	59	-11.537	22.407	21.809	1.00	20.25	IDIK 500
ATOM	409	CG	HIS	59	-11.767	22.867	23.218	1.00	21.97	IDIK 501
ATOM	410	ND1	HIS	59	-12.523	23.979	23.527	1.00	21.32	IDIK 502
ATOM	411	CD2	HIS	59	-11.350	22.356	24.400	1.00	18.14	IDIK 503
ATOM	412	CE2	HIS	59	-12.564	24.132	24.838	1.00	18.77	IDIK 504
ATOM	413	NE2	HIS	59	-11.860	23.161	25.390	1.00	19.93	IDIK 505
ATOM	414	N	GLY	60	-12.318	24.782	19.957	1.00	20.66	IDIK 506
ATOM	415	CA	GLY	60	-12.976	26.063	19.736	1.00	20.29	IDIK 507
ATOM	416	C	GLY	60	-13.950	26.442	20.847	1.00	21.31	IDIK 508
ATOM	417	O	GLY	60	-14.042	25.737	21.856	1.00	21.15	IDIK 509
ATOM	418	N	ALA	61	-14.669	27.549	20.659	1.00	20.16	IDIK 510
ATOM	419	CA	ALA	61	-15.664	28.047	21.618	1.00	20.00	IDIK 511
ATOM	420	C	ALA	61	-16.735	26.996	21.888	1.00	20.35	IDIK 512
ATOM	421	O	ALA	61	-17.247	26.366	20.954	1.00	21.69	IDIK 513
ATOM	422	CB	ALA	61	-16.326	29.320	21.079			

Figure 8/7

ATOM	433	NH2	ARG	62	-15.244	25.704	29.766	1.00	27.40	1DIK	525
ATOM	434	N	TYR	63	-20.193	25.619	24.726	1.00	23.53	1DIK	526
ATOM	435	CA	TYR	63	-21.280	26.004	25.615	1.00	25.54	1DIK	527
ATOM	436	C	TYR	63	-20.729	25.786	27.033	1.00	28.59	1DIK	528
ATOM	437	O	TYR	63	-19.646	25.206	27.200	1.00	28.67	1DIK	529
ATOM	438	CB	TYR	63	-22.481	25.082	25.394	1.00	24.63	1DIK	530
ATOM	439	CG	TYR	63	-23.192	25.300	24.082	1.00	29.77	1DIK	531
ATOM	440	CD1	TYR	63	-23.806	26.529	23.795	1.00	29.27	1DIK	532
ATOM	441	CD2	TYR	63	-23.237	24.290	23.116	1.00	27.48	1DIK	533
ATOM	442	CE1	TYR	63	-24.444	26.748	22.576	1.00	31.57	1DIK	534
ATOM	443	CE2	TYR	63	-23.867	24.495	21.895	1.00	26.46	1DIK	535
ATOM	444	CZ	TYR	63	-24.468	25.727	21.626	1.00	34.26	1DIK	536
ATOM	445	OH	TYR	63	-25.067	25.950	20.398	1.00	35.58	1DIK	537
ATOM	446	N	PRO	64	-21.444	26.254	28.076	1.00	31.03	1DIK	538
ATOM	447	CA	PRO	64	-20.879	26.003	29.407	1.00	31.84	1DIK	539
ATOM	448	C	PRO	64	-20.849	24.482	29.625	1.00	32.43	1DIK	540
ATOM	449	O	PRO	64	-21.547	23.728	28.932	1.00	30.67	1DIK	541
ATOM	450	CB	PRO	64	-21.891	26.670	30.342	1.00	27.12	1DIK	542
ATOM	451	CG	PRO	64	-22.524	27.706	29.487	1.00	30.89	1DIK	543
ATOM	452	CD	PRO	64	-22.706	27.004	28.181	1.00	27.90	1DIK	544
ATOM	453	N	THR	65	-20.042	24.011	30.564	1.00	35.27	1DIK	545
ATOM	454	CA	THR	65	-20.038	22.579	30.830	1.00	37.08	1DIK	546
ATOM	455	C	THR	65	-21.375	22.333	31.507	1.00	38.68	1DIK	547
ATOM	456	O	THR	65	-21.897	23.224	32.185	1.00	35.35	1DIK	548
ATOM	457	CB	THR	65	-18.897	22.170	31.774	1.00	35.91	1DIK	549
ATOM	458	OG1	THR	65	-18.997	22.906	32.999	1.00	40.63	1DIK	550
ATOM	459	CG2	THR	65	-17.544	22.438	31.116	1.00	35.54	1DIK	551
ATOM	460	N	ASP	66	-21.933	21.141	31.329	1.00	44.49	1DIK	552
ATOM	461	CA	ASP	66	-23.222	20.806	31.935	1.00	48.12	1DIK	553
ATOM	462	C	ASP	66	-23.305	21.205	33.418	1.00	48.96	1DIK	554
ATOM	463	O	ASP	66	-24.299	21.789	33.858	1.00	48.33	1DIK	555
ATOM	464	CB	ASP	66	-23.513	19.309	31.782	1.00	50.94	1DIK	556
ATOM	465	CG	ASP	66	-24.974	18.977	32.030	1.00	54.72	1DIK	557
ATOM	466	OD1	ASP	66	-25.838	19.495	31.280	1.00	55.38	1DIK	558
ATOM	467	OD2	ASP	66	-25.255	18.206	32.977	1.00	55.13	1DIK	559
ATOM	468	N	SER	67	-22.262	20.895	34.180	1.00	47.71	1DIK	560
ATOM	469	CA	SER	67	-22.233	21.247	35.587	1.00	46.65	1DIK	561
ATOM	470	C	SER	67	-22.525	22.751	35.796	1.00	45.82	1DIK	562
ATOM	471	O	SER	67	-23.477	23.102	36.501	1.00	47.90	1DIK	563
ATOM	472	CB	SER	67	-20.875	20.861	36.172	1.00	45.81	1DIK	564
ATOM	473	OC	SER	67	-20.769	21.285	37.516	1.00	51.18	1DIK	565
ATOM	474	N	LYS	68	-21.727	23.630	35.178	1.00	43.55	1DIK	566
ATOM	475	CA	LYS	68	-21.896	25.092	35.312	1.00	39.40	1DIK	567
ATOM	476	C	LYS	68	-23.201	25.626	34.753	1.00	37.75	1DIK	568
ATOM	477	O	LYS	68	-23.760	26.578	35.301	1.00	36.03	1DIK	569
ATOM	478	CB	LYS	68	-20.753	25.837	34.638	1.00	38.35	1DIK	570
ATOM	479	CG	LYS	68	-19.448	25.727	35.356	1.00	38.37	1DIK	571
ATOM	480	CD	LYS	68	-19.273	26.838	36.351	1.00	39.44	1DIK	572
ATOM	481	CE	LYS	68	-17.830	26.847	36.833	1.00	44.75	1DIK	573
ATOM	482	NZ	LYS	68	-17.376	28.222	37.198	1.00	52.53	1DIK	574
ATOM	483	N	GLY	69	-23.675	25.022	33.664	1.00	35.27	1DIK	575
ATOM	484	CA	GLY	69	-24.928	25.439	33.058	1.00	38.22	1DIK	576
ATOM	485	C	GLY	69	-26.073	25.358	34.054	1.00	41.32	1DIK	577
ATOM	486	O	GLY	69	-26.947	26.228	34.057	1.00	41.17	1DIK	578
ATOM	487	N	LYS	70	-26.059	24.313	34.891	1.00	42.89	1DIK	579
ATOM	488	CA	LYS	70	-27.071	24.092	35.934	1.00	44.02	1DIK	580
ATOM	489	C	LYS	70	-27.075	25.317	36.840	1.00	41.82	1DIK	581
ATOM	490	O	LYS	70	-28.110	25.959	37.043	1.00	42.10	1DIK	582
ATOM	491	CB	LYS	70	-26.717	22.892	36.835	1.00	49.51	1DIK	583
ATOM	492	CG	LYS	70	-26.624	21.513	36.195	1.00	53.72	1DIK	584
ATOM	493	CD	LYS	70	-27.976	20.920	35.867	1.00	56.10	1DIK	585
ATOM	494	CE	LYS	70	-27.822	19.444	35.549	1.00	56.46	1DIK	586
ATOM	495	NZ	LYS	70	-28.950	18.940	34.717	1.00	58.23	1DIK	587
ATOM	496	N	LYS	71	-25.901	25.625	37.382	1.00	34.23	1DIK	588
ATOM	497	CA	LYS	71	-25.735	26.752	38.278	1.00	32.70	1DIK	589
ATOM	498	C	LYS	71	-26.157	28.070	37.644	1.00	32.77	1DIK	590
ATOM	499	O	LYS	71	-26.839	28.867	38.283	1.00	34.19	1DIK	591
ATOM	500	CB	LYS	71	-24.294	26.814	38.743	1.00	34.32	1DIK	592
ATOM	501	CG	LYS	71	-23.848	25.549	39.465	1.00	38.15	1DIK	593
ATOM	502	CD	LYS	71	-22.365	25.606	39.758	1.00	42.92	1DIK	594
ATOM</td											

Figure 8/8

ATOM	518	CA	SER	73	-29.705	28.498	34.965	1.00	37.19	1DIK 610
ATOM	519	C	SER	73	-30.430	28.745	36.286	1.00	36.76	1DIK 611
ATOM	520	O	SER	73	-31.337	29.576	36.367	1.00	39.80	1DIK 612
ATOM	521	CB	SER	73	-30.100	27.133	34.421	1.00	37.82	1DIK 613
ATOM	522	OG	SER	73	-31.450	27.151	34.001	1.00	48.85	1DIK 614
ATOM	523	N	ALA	74	-30.027	28.017	37.321	1.00	36.25	1DIK 615
ATOM	524	CA	ALA	74	-30.627	28.143	38.645	1.00	32.75	1DIK 616
ATOM	525	C	ALA	74	-30.544	29.585	39.162	1.00	33.94	1DIK 617
ATOM	526	O	ALA	74	-31.544	30.156	39.607	1.00	37.43	1DIK 618
ATOM	527	CB	ALA	74	-29.929	27.196	39.612	1.00	27.83	1DIK 619
ATOM	528	N	LEU	75	-29.352	30.169	39.094	1.00	31.82	1DIK 620
ATOM	529	CA	LEU	75	-29.130	31.529	39.552	1.00	30.28	1DIK 621
ATOM	530	C	LEU	75	-30.043	32.526	38.855	1.00	32.18	1DIK 622
ATOM	531	O	LEU	75	-30.553	33.460	39.483	1.00	33.24	1DIK 623
ATOM	532	CB	LEU	75	-27.669	31.929	39.343	1.00	27.09	1DIK 624
ATOM	533	CG	LEU	75	-27.340	33.380	39.705	1.00	31.49	1DIK 625
ATOM	534	CD1	LEU	75	-27.680	33.616	41.182	1.00	32.22	1DIK 626
ATOM	535	CD2	LEU	75	-25.871	33.687	39.422	1.00	28.98	1DIK 627
ATOM	536	N	ILE	76	-30.253	32.334	37.559	1.00	34.42	1DIK 628
ATOM	537	CA	ILE	76	-31.107	33.235	36.800	1.00	35.51	1DIK 629
ATOM	538	C	ILE	76	-32.581	33.100	37.187	1.00	38.20	1DIK 630
ATOM	539	O	ILE	76	-33.287	34.104	37.290	1.00	37.73	1DIK 631
ATOM	540	CB	ILE	76	-30.897	33.040	35.271	1.00	35.44	1DIK 632
ATOM	541	CG1	ILE	76	-29.543	33.649	34.872	1.00	32.79	1DIK 633
ATOM	542	CG2	ILE	76	-32.051	33.665	34.467	1.00	30.04	1DIK 634
ATOM	543	CD1	ILE	76	-29.180	33.468	33.407	1.00	32.29	1DIK 635
ATOM	544	N	GLU	77	-33.050	31.876	37.409	1.00	41.02	1DIK 636
ATOM	545	CA	GLU	77	-34.440	31.683	37.801	1.00	45.17	1DIK 637
ATOM	546	C	GLU	77	-34.630	32.291	39.166	1.00	45.15	1DIK 638
ATOM	547	O	GLU	77	-35.655	32.926	39.434	1.00	46.76	1DIK 639
ATOM	548	CB	GLU	77	-34.800	30.209	37.861	1.00	51.95	1DIK 640
ATOM	549	CG	GLU	77	-34.891	29.564	36.499	1.00	66.31	1DIK 641
ATOM	550	CD	GLU	77	-35.578	28.203	36.531	1.00	74.99	1DIK 642
ATOM	551	OE1	GLU	77	-35.736	27.633	37.642	1.00	78.28	1DIK 643
ATOM	552	OE2	GLU	77	-35.960	27.702	35.443	1.00	79.43	1DIK 644
ATOM	553	N	GLU	78	-33.631	32.098	40.025	1.00	43.62	1DIK 645
ATOM	554	CA	GLU	78	-33.667	32.631	41.378	1.00	41.02	1DIK 646
ATOM	555	C	GLU	78	-33.758	34.155	41.364	1.00	38.09	1DIK 647
ATOM	556	O	GLU	78	-34.518	34.733	42.134	1.00	37.93	1DIK 648
ATOM	557	CB	GLU	78	-32.445	32.185	42.175	1.00	41.48	1DIK 649
ATOM	558	CG	GLU	78	-32.538	32.616	43.621	1.00	49.04	1DIK 650
ATOM	559	CD	GLU	78	-31.261	32.413	44.414	1.00	53.16	1DIK 651
ATOM	560	OE1	GLU	78	-30.551	31.404	44.174	1.00	56.49	1DIK 652
ATOM	561	OE2	GLU	78	-30.977	33.272	45.283	1.00	50.49	1DIK 653
ATOM	562	N	ILE	79	-32.989	34.810	40.501	1.00	36.46	1DIK 654
ATOM	563	CA	ILE	79	-33.059	36.265	40.400	1.00	37.33	1DIK 655
ATOM	564	C	ILE	79	-34.446	36.672	39.897	1.00	41.12	1DIK 656
ATOM	565	O	ILE	79	-35.034	37.648	40.374	1.00	43.28	1DIK 657
ATOM	566	CB	ILE	79	-32.003	36.829	39.418	1.00	36.22	1DIK 658
ATOM	567	CG1	ILE	79	-30.606	36.694	40.031	1.00	32.53	1DIK 659
ATOM	568	CG2	ILE	79	-32.341	38.300	39.057	1.00	30.60	1DIK 660
ATOM	569	CD1	ILE	79	-29.481	37.029	39.088	1.00	28.25	1DIK 661
ATOM	570	N	GLN	80	-34.965	35.918	38.934	1.00	41.53	1DIK 662
ATOM	571	CA	GLN	80	-36.276	36.201	38.375	1.00	43.98	1DIK 663
ATOM	572	C	GLN	80	-37.399	36.074	39.392	1.00	48.10	1DIK 664
ATOM	573	O	GLN	80	-38.450	36.687	39.228	1.00	51.13	1DIK 665
ATOM	574	CB	GLN	80	-36.549	35.290	37.186	1.00	40.14	1DIK 666
ATOM	575	CG	GLN	80	-35.828	35.733	35.933	1.00	41.38	1DIK 667
ATOM	576	CD	GLN	80	-35.983	34.751	34.792	1.00	42.01	1DIK 668
ATOM	577	OE1	GLN	80	-36.303	33.583	35.000	1.00	43.95	1DIK 669
ATOM	578	NE2	GLN	80	-35.753	35.220	33.577	1.00	40.77	1DIK 670
ATOM	579	N	GLN	81	-37.186	35.281	40.437	1.00	51.52	1DIK 671
ATOM	580	CA	GLN	81	-38.205	35.105	41.468	1.00	54.70	1DIK 672
ATOM	581	C	GLN	81	-38.099	36.109	42.611	1.00	54.45	1DIK 673
ATOM	582	O	GLN	81	-39.089	36.717	43.004	1.00	57.66	1DIK 674
ATOM	583	CB	GLN	81	-38.139	33.699	42.050	1.00	58.18	1DIK 675
ATOM	584	CG	GLN	81	-38.560	32.607	41.093	1.00	70.29	1DIK 676
ATOM	585	CD	GLN	81	-38.505	31.233	41.746	1.00	78.03	1DIK 677
ATOM	586	OE1	GLN	81	-39.099	31.014	42.809	1.00	80.87	1DIK 678
ATOM	587	NE2	GLN	81	-37.790	30.300	41.116	1.00	80.03	1DIK 679
ATOM	588	N	ASN	82	-36.896	36.280	43.138	1.00	52.58	1DIK 680
ATOM	589	CA	ASN	82	-36.668	37.179	44.263	1.00	52.84	1DIK 681
ATOM	590	C	ASN	82	-36.717	38.688	44.013	1.00		

Figure 8/9

ATOM	603	C	THR	84	-39.170	44.025	41.730	1.00	60.59	1DIK 695
ATOM	604	O	THR	84	-40.212	44.256	41.116	1.00	63.43	1DIK 696
ATOM	605	CB	THR	84	-39.452	43.835	44.223	1.00	61.01	1DIK 697
ATOM	606	OG1	THR	84	-38.308	44.638	44.574	1.00	61.94	1DIK 698
ATOM	607	CG2	THR	84	-39.786	42.871	45.375	1.00	57.54	1DIK 699
ATOM	608	N	THR	85	-38.011	44.595	41.410	1.00	60.26	1DIK 700
ATOM	609	CA	THR	85	-37.923	45.550	40.309	1.00	61.94	1DIK 701
ATOM	610	C	THR	85	-36.844	45.254	39.271	1.00	60.00	1DIK 702
ATOM	611	O	THR	85	-35.710	44.923	39.608	1.00	58.14	1DIK 703
ATOM	612	CB	THR	85	-37.714	46.973	40.844	1.00	64.54	1DIK 704
ATOM	613	OG1	THR	85	-36.901	46.916	42.027	1.00	68.74	1DIK 705
ATOM	614	CG2	THR	85	-39.062	47.627	41.167	1.00	64.69	1DIK 706
ATOM	615	N	PHE	86	-37.217	45.380	38.003	1.00	59.68	1DIK 707
ATOM	616	CA	PHE	86	-36.301	45.143	36.895	1.00	59.09	1DIK 708
ATOM	617	C	PHE	86	-36.308	46.366	35.988	1.00	58.32	1DIK 709
ATOM	618	O	PHE	86	-36.829	46.298	34.880	1.00	58.58	1DIK 710
ATOM	619	CB	PHE	86	-36.752	43.940	36.055	1.00	59.17	1DIK 711
ATOM	620	CG	PHE	86	-36.747	42.633	36.787	1.00	60.12	1DIK 712
ATOM	621	CD1	PHE	86	-35.566	41.917	36.952	1.00	60.09	1DIK 713
ATOM	622	CD2	PHE	86	-37.928	42.103	37.294	1.00	58.71	1DIK 714
ATOM	623	CE1	PHE	86	-35.564	40.685	37.614	1.00	62.46	1DIK 715
ATOM	624	CE2	PHE	86	-37.939	40.873	37.957	1.00	59.49	1DIK 716
ATOM	625	CZ	PHE	86	-36.756	40.162	38.117	1.00	59.88	1DIK 717
ATOM	626	N	ASP	87	-35.743	47.484	36.432	1.00	59.28	1DIK 718
ATOM	627	CA	ASP	87	-35.745	48.672	35.576	1.00	61.03	1DIK 719
ATOM	628	C	ASP	87	-34.390	49.050	34.977	1.00	58.67	1DIK 720
ATOM	629	O	ASP	87	-33.331	48.696	35.503	1.00	56.33	1DIK 721
ATOM	630	CB	ASP	87	-36.376	49.882	36.294	1.00	67.39	1DIK 722
ATOM	631	CG	ASP	87	-35.731	50.181	37.634	1.00	74.12	1DIK 723
ATOM	632	OD1	ASP	87	-34.542	50.581	37.654	1.00	77.08	1DIK 724
ATOM	633	OD2	ASP	87	-36.422	50.017	38.670	1.00	76.76	1DIK 725
ATOM	634	N	GLY	88	-34.438	49.775	33.864	1.00	56.11	1DIK 726
ATOM	635	CA	GLY	88	-33.223	50.193	33.195	1.00	52.64	1DIK 727
ATOM	636	C	GLY	88	-32.521	49.004	32.565	1.00	50.66	1DIK 728
ATOM	637	O	GLY	88	-33.161	48.140	31.950	1.00	48.22	1DIK 729
ATOM	638	N	LYS	89	-31.202	48.957	32.734	1.00	47.80	1DIK 730
ATOM	639	CA	LYS	89	-30.376	47.885	32.188	1.00	45.18	1DIK 731
ATOM	640	C	LYS	89	-30.681	46.482	32.744	1.00	44.09	1DIK 732
ATOM	641	O	LYS	89	-30.087	45.504	32.301	1.00	46.90	1DIK 733
ATOM	642	CB	LYS	89	-28.898	48.222	32.390	1.00	42.58	1DIK 734
ATOM	643	CG	LYS	89	-28.530	48.500	33.828	1.00	47.71	1DIK 735
ATOM	644	CD	LYS	89	-27.068	48.905	33.973	1.00	54.98	1DIK 736
ATOM	645	CE	LYS	89	-26.737	49.253	35.426	1.00	56.55	1DIK 737
ATOM	646	NZ	LYS	89	-25.293	49.611	35.610	1.00	61.03	1DIK 738
ATOM	647	N	TYR	90	-31.594	46.382	33.705	1.00	38.46	1DIK 739
ATOM	648	CA	TYR	90	-31.959	45.095	34.277	1.00	35.36	1DIK 740
ATOM	649	C	TYR	90	-33.269	44.568	33.699	1.00	38.19	1DIK 741
ATOM	650	O	TYR	90	-33.709	43.469	34.042	1.00	36.65	1DIK 742
ATOM	651	CB	TYR	90	-32.122	45.220	35.781	1.00	32.46	1DIK 743
ATOM	652	CG	TYR	90	-30.873	45.633	36.506	1.00	31.81	1DIK 744
ATOM	653	CD1	TYR	90	-29.901	44.693	36.851	1.00	32.85	1DIK 745
ATOM	654	CD2	TYR	90	-30.668	46.959	36.866	1.00	32.53	1DIK 746
ATOM	655	CE1	TYR	90	-28.754	45.066	37.539	1.00	29.82	1DIK 747
ATOM	656	CE2	TYR	90	-29.528	47.351	37.553	1.00	32.39	1DIK 748
ATOM	657	CZ	TYR	90	-28.574	46.400	37.887	1.00	34.71	1DIK 749
ATOM	658	OH	TYR	90	-27.446	46.792	38.565	1.00	31.33	1DIK 750
ATOM	659	N	ALA	91	-33.891	45.351	32.820	1.00	41.63	1DIK 751
ATOM	660	CA	ALA	91	-35.168	44.978	32.218	1.00	40.63	1DIK 752
ATOM	661	C	ALA	91	-35.159	43.631	31.510	1.00	40.55	1DIK 753
ATOM	662	O	ALA	91	-36.105	42.858	31.641	1.00	41.26	1DIK 754
ATOM	663	CB	ALA	91	-35.632	46.069	31.262	1.00	40.02	1DIK 755
ATOM	664	N	PHE	92	-34.097	43.340	30.763	1.00	41.42	1DIK 756
ATOM	665	CA	PHE	92	-34.010	42.069	30.036	1.00	39.95	1DIK 757
ATOM	666	C	PHE	92	-34.164	40.849	30.938	1.00	38.42	1DIK 758
ATOM	667	O	PHE	92	-34.726	39.836	30.526	1.00	36.46	1DIK 759
ATOM	668	CB	PHE	92	-32.677	41.972	29.287	1.00	38.12	1DIK 760
ATOM	669	CG	PHE	92	-31.499	41.624	30.163	1.00	36.18	1DIK 761
ATOM	670	CD1	PHE	92	-30.861	42.606	30.919	1.00	32.76	1DIK 762
ATOM	671	CD2	PHE	92	-31.018	40.314	30.215	1.00	34.57	1DIK 763
ATOM	672	CE1	PHE	92	-29.760	42.297	31.713	1.00	34.09	1DIK 764
ATOM	673	CE2	PHE	92	-29.917	39.991	31.006	1.00	33.52	1DIK 765
ATOM	674	CZ	PHE	92	-29.284	40.988	31.759	1.00	34.32	1DIK 766
ATOM	675	N	LEU	93	-33.657	40.961	32.164	1.00	39.65	1DIK

Figure 8/10

ATOM	688	CG	LYS	94	-39.736	40.899	34.322	1.00	66.52	1DIK 780
ATOM	689	CD	LYS	94	-40.436	42.236	34.556	1.00	71.87	1DIK 781
ATOM	690	CE	LYS	94	-41.818	42.031	35.189	1.00	75.09	1DIK 782
ATOM	691	NZ	LYS	94	-42.493	43.320	35.533	1.00	75.30	1DIK 783
ATOM	692	N	THR	95	-37.549	38.687	31.643	1.00	52.52	1DIK 784
ATOM	693	CA	THR	95	-37.991	37.622	30.748	1.00	50.56	1DIK 785
ATOM	694	C	THR	95	-36.902	36.850	30.009	1.00	49.46	1DIK 786
ATOM	695	O	THR	95	-37.177	36.258	28.960	1.00	48.63	1DIK 787
ATOM	696	CB	THR	95	-38.962	38.168	29.700	1.00	52.17	1DIK 788
ATOM	697	OG1	THR	95	-38.366	39.295	29.039	1.00	48.18	1DIK 789
ATOM	698	CG2	THR	95	-40.272	38.574	30.357	1.00	54.41	1DIK 790
ATOM	699	N	TYR	96	-35.676	36.855	30.531	1.00	47.27	1DIK 791
ATOM	700	CA	TYR	96	-34.582	36.119	29.894	1.00	44.27	1DIK 792
ATOM	701	C	TYR	96	-34.863	34.613	29.997	1.00	44.70	1DIK 793
ATOM	702	O	TYR	96	-35.227	34.107	31.060	1.00	43.58	1DIK 794
ATOM	703	CB	TYR	96	-33.236	36.456	30.550	1.00	37.81	1DIK 795
ATOM	704	CG	TYR	96	-32.071	35.699	29.957	1.00	34.72	1DIK 796
ATOM	705	CD1	TYR	96	-31.362	36.208	28.866	1.00	38.16	1DIK 797
ATOM	706	CD2	TYR	96	-31.683	34.465	30.474	1.00	35.36	1DIK 798
ATOM	707	CE1	TYR	96	-30.290	35.499	28.302	1.00	37.21	1DIK 799
ATOM	708	CE2	TYR	96	-30.620	33.747	29.923	1.00	37.79	1DIK 800
ATOM	709	CZ	TYR	96	-29.929	34.269	28.839	1.00	39.34	1DIK 801
ATOM	710	OH	TYR	96	-28.882	33.557	28.303	1.00	37.35	1DIK 802
ATOM	711	N	ASN	97	-34.694	33.903	28.888	1.00	43.16	1DIK 803
ATOM	712	CA	ASN	97	-34.937	32.471	28.859	1.00	45.14	1DIK 804
ATOM	713	C	ASN	97	-33.617	31.744	28.554	1.00	45.53	1DIK 805
ATOM	714	O	ASN	97	-33.097	31.838	27.436	1.00	46.50	1DIK 806
ATOM	715	CB	ASN	97	-35.988	32.167	27.788	1.00	50.43	1DIK 807
ATOM	716	CG	ASN	97	-36.536	30.758	27.895	1.00	58.07	1DIK 808
ATOM	717	OD1	ASN	97	-36.630	30.191	28.991	1.00	62.08	1DIK 809
ATOM	718	ND2	ASN	97	-36.905	30.179	26.755	1.00	59.47	1DIK 810
ATOM	719	N	TYR	98	-33.079	31.035	29.550	1.00	42.20	1DIK 811
ATOM	720	CA	TYR	98	-31.814	30.308	29.413	1.00	39.67	1DIK 812
ATOM	721	C	TYR	98	-31.937	29.149	28.430	1.00	39.43	1DIK 813
ATOM	722	O	TYR	98	-32.589	28.156	28.719	1.00	42.93	1DIK 814
ATOM	723	CB	TYR	98	-31.357	29.772	30.775	1.00	35.56	1DIK 815
ATOM	724	CG	TYR	98	-29.955	29.201	30.763	1.00	34.67	1DIK 816
ATOM	725	CD1	TYR	98	-29.720	27.862	30.440	1.00	33.36	1DIK 817
ATOM	726	CD2	TYR	98	-28.857	30.004	31.067	1.00	30.84	1DIK 818
ATOM	727	CE1	TYR	98	-28.421	27.343	30.421	1.00	33.02	1DIK 819
ATOM	728	CE2	TYR	98	-27.564	29.496	31.053	1.00	31.68	1DIK 820
ATOM	729	CZ	TYR	98	-27.351	28.167	30.731	1.00	32.17	1DIK 821
ATOM	730	OH	TYR	98	-26.071	27.673	30.742	1.00	31.22	1DIK 822
ATOM	731	N	SER	99	-31.304	29.267	27.272	1.00	41.23	1DIK 823
ATOM	732	CA	SER	99	-31.395	28.211	26.277	1.00	42.13	1DIK 824
ATOM	733	C	SER	99	-30.043	27.782	25.699	1.00	41.05	1DIK 825
ATOM	734	O	SER	99	-29.972	27.293	24.572	1.00	39.39	1DIK 826
ATOM	735	CB	SER	99	-32.340	28.645	25.148	1.00	43.93	1DIK 827
ATOM	736	OG	SER	99	-31.869	29.828	24.518	1.00	44.91	1DIK 828
ATOM	737	N	LEU	100	-28.970	27.964	26.464	1.00	38.89	1DIK 829
ATOM	738	CA	LEU	100	-27.647	27.561	25.999	1.00	36.71	1DIK 830
ATOM	739	C	LEU	100	-27.555	26.038	26.067	1.00	35.82	1DIK 831
ATOM	740	O	LEU	100	-28.181	25.425	26.932	1.00	37.24	1DIK 832
ATOM	741	CB	LEU	100	-26.548	28.175	26.878	1.00	33.03	1DIK 833
ATOM	742	CG	LEU	100	-26.381	29.694	26.799	1.00	33.85	1DIK 834
ATOM	743	CD1	LEU	100	-25.272	30.149	27.725	1.00	30.27	1DIK 835
ATOM	744	CD2	LEU	100	-26.063	30.090	25.375	1.00	33.01	1DIK 836
ATOM	745	N	GLY	101	-26.789	25.437	25.153	1.00	34.71	1DIK 837
ATOM	746	CA	GLY	101	-26.585	23.999	25.169	1.00	29.13	1DIK 838
ATOM	747	C	GLY	101	-25.572	23.673	26.270	1.00	31.41	1DIK 839
ATOM	748	O	GLY	101	-25.410	24.443	27.227	1.00	28.98	1DIK 840
ATOM	749	N	ALA	102	-24.875	22.547	26.163	1.00	30.11	1DIK 841
ATOM	750	CA	ALA	102	-23.892	22.208	27.180	1.00	29.75	1DIK 842
ATOM	751	C	ALA	102	-22.745	21.409	26.581	1.00	29.60	1DIK 843
ATOM	752	O	ALA	102	-22.943	20.675	25.622	1.00	32.26	1DIK 844
ATOM	753	CB	ALA	102	-24.556	21.423	28.318	1.00	26.45	1DIK 845
ATOM	754	N	ASP	103	-21.553	21.578	27.148	1.00	29.83	1DIK 846
ATOM	755	CA	ASP	103	-20.329	20.868	26.756	1.00	31.04	1DIK 847
ATOM	756	C	ASP	103	-19.817	20.909	25.318	1.00	29.41	1DIK 848
ATOM	757	O	ASP	103	-18.603	20.919	25.093	1.00	26.94	1DIK 849
ATOM	758	CB	ASP	103	-20.425	19.391	27.175	1.00	32.82	1DIK 850
ATOM	759	CG	ASP	103	-20.685	19.213	28.665	1.00	37.87	1DIK 851
ATOM	760	OD1	ASP	103	-19.906	19.738	2			

Figure 8/11

ATOM	773	O	LEU	105	-20.626	23.116	19.531	1.00	27.73	1DIK 865
ATOM	774	CB	LEU	105	-17.668	22.327	19.334	1.00	27.40	1DIK 866
ATOM	775	CG	LEU	105	-16.474	23.040	18.736	1.00	27.83	1DIK 867
ATOM	776	CD1	LEU	105	-15.518	23.368	19.855	1.00	33.80	1DIK 868
ATOM	777	CD2	LEU	105	-15.790	22.162	17.716	1.00	27.39	1DIK 869
ATOM	778	N	THR	106	-19.599	25.075	19.917	1.00	28.75	1DIK 870
ATOM	779	CA	THR	106	-20.714	25.848	19.358	1.00	28.71	1DIK 871
ATOM	780	C	THR	106	-20.462	26.060	17.858	1.00	31.52	1DIK 872
ATOM	781	O	THR	106	-19.338	25.863	17.369	1.00	32.15	1DIK 873
ATOM	782	CB	THR	106	-20.849	27.256	20.001	1.00	29.41	1DIK 874
ATOM	783	OG1	THR	106	-19.691	28.044	19.698	1.00	28.94	1DIK 875
ATOM	784	CG2	THR	106	-21.034	27.164	21.496	1.00	27.82	1DIK 876
ATOM	785	N	PRO	107	-21.503	26.448	17.098	1.00	30.71	1DIK 877
ATOM	786	CA	PRO	107	-21.312	26.680	15.658	1.00	28.88	1DIK 878
ATOM	787	C	PRO	107	-20.169	27.693	15.406	1.00	27.50	1DIK 879
ATOM	788	O	PRO	107	-19.381	27.531	14.464	1.00	30.80	1DIK 880
ATOM	789	CB	PRO	107	-22.679	27.203	15.218	1.00	25.78	1DIK 881
ATOM	790	CG	PRO	107	-23.610	26.495	16.163	1.00	27.66	1DIK 882
ATOM	791	CD	PRO	107	-22.910	26.662	17.481	1.00	28.45	1DIK 883
ATOM	792	N	PHE	108	-20.082	28.727	16.245	1.00	23.11	1DIK 884
ATOM	793	CA	PHE	108	-19.015	29.729	16.151	1.00	22.62	1DIK 885
ATOM	794	C	PHE	108	-17.644	29.059	16.383	1.00	25.28	1DIK 886
ATOM	795	O	PHE	108	-16.657	29.356	15.670	1.00	25.00	1DIK 887
ATOM	796	CB	PHE	108	-19.226	30.837	17.195	1.00	20.26	1DIK 888
ATOM	797	CG	PHE	108	-18.063	31.794	17.312	1.00	25.13	1DIK 889
ATOM	798	CD1	PHE	108	-17.819	32.743	16.325	1.00	24.81	1DIK 890
ATOM	799	CD2	PHE	108	-17.196	31.737	18.410	1.00	28.22	1DIK 891
ATOM	800	CE1	PHE	108	-16.726	33.617	16.430	1.00	26.50	1DIK 892
ATOM	801	CE2	PHE	108	-16.101	32.609	18.521	1.00	25.64	1DIK 893
ATOM	802	CZ	PHE	108	-15.868	33.546	17.531	1.00	22.77	1DIK 894
ATOM	803	N	GLY	109	-17.597	28.164	17.380	1.00	21.53	1DIK 895
ATOM	804	CA	GLY	109	-16.383	27.428	17.704	1.00	21.31	1DIK 896
ATOM	805	C	GLY	109	-15.917	26.535	16.562	1.00	22.06	1DIK 897
ATOM	806	O	GLY	109	-14.713	26.384	16.338	1.00	22.23	1DIK 898
ATOM	807	N	GLU	110	-16.869	25.941	15.842	1.00	20.87	1DIK 899
ATOM	808	CA	GLU	110	-16.565	25.108	14.687	1.00	18.70	1DIK 900
ATOM	809	C	GLU	110	-15.908	25.975	13.623	1.00	19.56	1DIK 901
ATOM	810	O	GLU	110	-14.895	25.590	13.019	1.00	20.43	1DIK 902
ATOM	811	CB	GLU	110	-17.843	24.513	14.123	1.00	19.80	1DIK 903
ATOM	812	CG	GLU	110	-18.563	23.605	15.104	1.00	22.70	1DIK 904
ATOM	813	CD	GLU	110	-19.803	22.983	14.520	1.00	23.25	1DIK 905
ATOM	814	OE1	GLU	110	-20.346	23.513	13.524	1.00	27.96	1DIK 906
ATOM	815	OE2	GLU	110	-20.237	21.955	15.063	1.00	26.17	1DIK 907
ATOM	816	N	GLN	111	-16.489	27.153	13.402	1.00	18.95	1DIK 908
ATOM	817	CA	GLN	111	-15.963	28.094	12.427	1.00	20.74	1DIK 909
ATOM	818	C	GLN	111	-14.541	28.523	12.791	1.00	21.64	1DIK 910
ATOM	819	O	GLN	111	-13.679	28.651	11.908	1.00	21.26	1DIK 911
ATOM	820	CB	GLN	111	-16.868	29.321	12.319	1.00	26.01	1DIK 912
ATOM	821	CG	GLN	111	-16.527	30.222	11.144	1.00	32.20	1DIK 913
ATOM	822	CD	GLN	111	-16.503	29.455	9.825	1.00	37.67	1DIK 914
ATOM	823	OE1	GLN	111	-17.440	28.718	9.511	1.00	42.78	1DIK 915
ATOM	824	NE2	GLN	111	-15.432	29.620	9.051	1.00	34.61	1DIK 916
ATOM	825	N	GLU	112	-14.292	28.743	14.084	1.00	20.80	1DIK 917
ATOM	826	CA	GLU	112	-12.960	29.137	14.550	1.00	19.26	1DIK 918
ATOM	827	C	GLU	112	-11.875	28.135	14.133	1.00	19.50	1DIK 919
ATOM	828	O	GLU	112	-10.777	28.537	13.705	1.00	14.92	1DIK 920
ATOM	829	CB	GLU	112	-12.923	29.262	16.075	1.00	19.60	1DIK 921
ATOM	830	CG	GLU	112	-13.535	30.522	16.669	1.00	19.22	1DIK 922
ATOM	831	CD	GLU	112	-13.276	30.607	18.157	1.00	19.02	1DIK 923
ATOM	832	OE1	GLU	112	-13.712	29.691	18.878	1.00	19.03	1DIK 924
ATOM	833	OE2	GLU	112	-12.636	31.576	18.611	1.00	19.54	1DIK 925
ATOM	834	N	LEU	113	-12.177	26.841	14.262	1.00	15.87	1DIK 926
ATOM	835	CA	LEU	113	-11.213	25.803	13.908	1.00	18.95	1DIK 927
ATOM	836	C	LEU	113	-11.023	25.666	12.398	1.00	19.66	1DIK 928
ATOM	837	O	LEU	113	-9.907	25.411	11.929	1.00	19.09	1DIK 929
ATOM	838	CB	LEU	113	-11.592	24.471	14.559	1.00	19.94	1DIK 930
ATOM	839	CG	LEU	113	-11.016	24.283	15.966	1.00	19.61	1DIK 931
ATOM	840	CD1	LEU	113	-9.550	23.910	15.842	1.00	17.82	1DIK 932
ATOM	841	CD2	LEU	113	-11.190	25.552	16.819	1.00	15.58	1DIK 933
ATOM	842	N	VAL	114	-12.104	25.840	11.641	1.00	20.06	1DIK 934
ATOM	843	CA	VAL	114	-12.020	25.801	10.183	1.00	18.34	1DIK 935
ATOM	844	C	VAL	114	-11.039	26.916	9.779	1.00	19.73	1DIK 936
ATOM	84									

Figure 8/12

ATOM	858	CA	SER	116	-7.358	27.966	12.004	1.00	20.45	1DIK 950
ATOM	859	C	SER	116	-6.696	26.987	11.000	1.00	20.54	1DIK 951
ATOM	860	O	SER	116	-5.489	27.078	10.725	1.00	19.21	1DIK 952
ATOM	861	CB	SER	116	-7.463	27.330	13.407	1.00	20.16	1DIK 953
ATOM	862	OG	SER	116	-6.199	27.086	13.987	1.00	15.09	1DIK 954
ATOM	863	N	GLY	117	-7.484	26.059	10.458	1.00	17.37	1DIK 955
ATOM	864	CA	GLY	117	-6.963	25.112	9.485	1.00	18.31	1DIK 956
ATOM	865	C	GLY	117	-6.507	25.807	8.209	1.00	19.33	1DIK 957
ATOM	866	O	GLY	117	-5.468	25.455	7.647	1.00	22.20	1DIK 958
ATOM	867	N	ILE	118	-7.294	26.784	7.759	1.00	18.87	1DIK 959
ATOM	868	CA	ILE	118	-6.998	27.585	6.567	1.00	19.05	1DIK 960
ATOM	869	C	ILE	118	-5.690	28.347	6.739	1.00	19.38	1DIK 961
ATOM	870	O	ILE	118	-4.831	28.365	5.848	1.00	20.03	1DIK 962
ATOM	871	CB	ILE	118	-8.105	28.640	6.316	1.00	18.22	1DIK 963
ATOM	872	CG1	ILE	118	-9.392	27.959	5.860	1.00	16.45	1DIK 964
ATOM	873	CG2	ILE	118	-7.627	29.608	5.310	1.00	13.65	1DIK 965
ATOM	874	CD1	ILE	118	-10.549	28.901	5.792	1.00	12.46	1DIK 966
ATOM	875	N	LYS	119	-5.555	28.979	7.900	1.00	21.72	1DIK 967
ATOM	876	CA	LYS	119	-4.381	29.775	8.225	1.00	21.99	1DIK 968
ATOM	877	C	LYS	119	-3.095	28.955	8.340	1.00	22.12	1DIK 969
ATOM	878	O	LYS	119	-2.034	29.404	7.881	1.00	22.21	1DIK 970
ATOM	879	CB	LYS	119	-4.636	30.574	9.503	1.00	22.43	1DIK 971
ATOM	880	CG	LYS	119	-3.536	31.557	9.789	1.00	27.62	1DIK 972
ATOM	881	CD	LYS	119	-4.020	32.690	10.649	1.00	29.86	1DIK 973
ATOM	882	CE	LYS	119	-2.986	33.798	10.646	1.00	29.14	1DIK 974
ATOM	883	NZ	LYS	119	-3.311	34.827	11.667	1.00	30.24	1DIK 975
ATOM	884	N	PHE	120	-3.191	27.765	8.942	1.00	19.44	1DIK 976
ATOM	885	CA	PHE	120	-2.034	26.879	9.084	1.00	20.52	1DIK 977
ATOM	886	C	PHE	120	-1.561	26.429	7.694	1.00	22.99	1DIK 978
ATOM	887	O	PHE	120	-0.355	26.404	7.415	1.00	21.56	1DIK 979
ATOM	888	CB	PHE	120	-2.381	25.647	9.927	1.00	18.62	1DIK 980
ATOM	889	CG	PHE	120	-1.208	24.727	10.163	1.00	25.65	1DIK 981
ATOM	890	CD1	PHE	120	-0.192	25.083	11.059	1.00	23.32	1DIK 982
ATOM	891	CD2	PHE	120	-1.114	23.504	9.493	1.00	25.43	1DIK 983
ATOM	892	CE1	PHE	120	0.894	24.243	11.284	1.00	18.73	1DIK 984
ATOM	893	CE2	PHE	120	-0.025	22.651	9.712	1.00	22.55	1DIK 985
ATOM	894	CZ	PHE	120	0.981	23.021	10.610	1.00	20.53	1DIK 986
ATOM	895	N	TYR	121	-2.515	26.074	6.830	1.00	20.17	1DIK 987
ATOM	896	CA	TYR	121	-2.179	25.656	5.482	1.00	19.95	1DIK 988
ATOM	897	C	TYR	121	-1.450	26.766	4.718	1.00	21.59	1DIK 989
ATOM	898	O	TYR	121	-0.402	26.528	4.112	1.00	19.41	1DIK 990
ATOM	899	CB	TYR	121	-3.427	25.271	4.668	1.00	19.72	1DIK 991
ATOM	900	CG	TYR	121	-3.029	24.865	3.265	1.00	20.01	1DIK 992
ATOM	901	CD1	TYR	121	-2.859	25.819	2.240	1.00	18.79	1DIK 993
ATOM	902	CD2	TYR	121	-2.721	23.537	2.983	1.00	20.66	1DIK 994
ATOM	903	CE1	TYR	121	-2.381	25.445	0.976	1.00	19.33	1DIK 995
ATOM	904	CE2	TYR	121	-2.246	23.152	1.730	1.00	23.50	1DIK 996
ATOM	905	CZ	TYR	121	-2.074	24.097	0.737	1.00	23.64	1DIK 997
ATOM	906	OH	TYR	121	-1.593	23.670	-0.472	1.00	22.79	1DIK 998
ATOM	907	N	GLN	122	-2.021	27.969	4.734	1.00	23.17	1DIK 999
ATOM	908	CA	GLN	122	-1.447	29.104	4.022	1.00	22.67	1DIK 1000
ATOM	909	C	GLN	122	-0.085	29.549	4.527	1.00	22.41	1DIK 1001
ATOM	910	O	GLN	122	0.799	29.860	3.735	1.00	25.99	1DIK 1002
ATOM	911	CB	GLN	122	-2.387	30.296	4.071	1.00	26.42	1DIK 1003
ATOM	912	CG	GLN	122	-3.691	30.133	3.323	1.00	27.92	1DIK 1004
ATOM	913	CD	GLN	122	-4.623	31.333	3.531	1.00	34.41	1DIK 1005
ATOM	914	OE1	GLN	122	-4.531	32.066	4.537	1.00	33.16	1DIK 1006
ATOM	915	NE2	GLN	122	-5.528	31.538	2.582	1.00	36.14	1DIK 1007
ATOM	916	N	ARG	123	0.089	29.586	5.841	1.00	22.55	1DIK 1008
ATOM	917	CA	ARG	123	1.359	30.011	6.416	1.00	21.19	1DIK 1009
ATOM	918	C	ARG	123	2.541	29.106	6.012	1.00	23.05	1DIK 1010
ATOM	919	O	ARG	123	3.652	29.582	5.785	1.00	23.96	1DIK 1011
ATOM	920	CB	ARG	123	1.225	30.083	7.947	1.00	20.65	1DIK 1012
ATOM	921	CG	ARG	123	2.485	30.519	8.653	1.00	19.56	1DIK 1013
ATOM	922	CD	ARG	123	2.297	30.672	10.146	1.00	21.87	1DIK 1014
ATOM	923	NE	ARG	123	3.580	30.971	10.789	1.00	24.63	1DIK 1015
ATOM	924	CZ	ARG	123	4.173	32.174	10.802	1.00	28.06	1DIK 1016
ATOM	925	NH1	ARG	123	3.605	33.236	10.232	1.00	18.64	1DIK 1017
ATOM	926	NH2	ARG	123	5.349	32.319	11.402	1.00	24.13	1DIK 1018
ATOM	927	N	TYR	124	2.298	27.803	5.915	1.00	24.21	1DIK 1019
ATOM	928	CA	TYR	124	3.346	26.852	5.572	1.00	24.48	1DIK 1020
ATOM	929	C	TYR	124	3.125	26.182	4.222	1.00	26.16	1DIK 1021
ATOM	930	O	TYR	124	3.486	25.016	4.049	1.00	24.40	1DIK 1022
ATOM	93									

Figure 8/13

ATOM	943	CB	GLU	125	1.875	27.566	0.985	1.00	35.88	1DIK1035
ATOM	944	CG	GLU	125	1.226	27.149	-0.360	1.00	46.46	1DIK1036
ATOM	945	CD	GLU	125	2.239	26.814	-1.475	1.00	54.36	1DIK1037
ATOM	946	OE1	GLU	125	3.343	27.412	-1.491	1.00	58.38	1DIK1038
ATOM	947	OE2	GLU	125	1.937	25.955	-2.343	1.00	54.70	1DIK1039
ATOM	948	N	SER	126	4.583	25.929	1.383	1.00	28.00	1DIK1040
ATOM	949	CA	SER	126	5.651	25.161	0.755	1.00	31.00	1DIK1041
ATOM	950	C	SER	126	5.733	23.711	1.249	1.00	31.74	1DIK1042
ATOM	951	O	SER	126	6.217	22.831	0.525	1.00	32.26	1DIK1043
ATOM	952	CB	SER	126	6.992	25.881	0.936	1.00	33.57	1DIK1044
ATOM	953	OG	SER	126	7.256	26.134	2.308	1.00	41.28	1DIK1045
ATOM	954	N	LEU	127	5.262	23.476	2.477	1.00	28.17	1DIK1046
ATOM	955	CA	LEU	127	5.246	22.148	3.087	1.00	23.13	1DIK1047
ATOM	956	C	LEU	127	3.879	21.466	2.981	1.00	22.92	1DIK1048
ATOM	957	O	LEU	127	3.781	20.304	2.584	1.00	24.92	1DIK1049
ATOM	958	CB	LEU	127	5.601	22.236	4.569	1.00	21.37	1DIK1050
ATOM	959	CG	LEU	127	7.017	22.618	4.969	1.00	24.27	1DIK1051
ATOM	960	CD1	LEU	127	7.125	22.582	6.485	1.00	17.41	1DIK1052
ATOM	961	CD2	LEU	127	8.006	21.652	4.316	1.00	20.13	1DIK1053
ATOM	962	N	THR	128	2.833	22.198	3.352	1.00	22.22	1DIK1054
ATOM	963	CA	THR	128	1.461	21.701	3.357	1.00	21.36	1DIK1055
ATOM	964	C	THR	128	0.935	21.259	1.989	1.00	25.64	1DIK1056
ATOM	965	O	THR	128	0.016	20.429	1.907	1.00	26.78	1DIK1057
ATOM	966	CB	THR	128	0.502	22.765	3.941	1.00	18.91	1DIK1058
ATOM	967	OG1	THR	128	0.687	24.008	3.248	1.00	16.25	1DIK1059
ATOM	968	CG2	THR	128	0.771	22.971	5.413	1.00	8.45	1DIK1060
ATOM	969	N	ARG	129	1.510	21.803	0.917	1.00	27.58	1DIK1061
ATOM	970	CA	ARG	129	1.070	21.436	-0.423	1.00	27.49	1DIK1062
ATOM	971	C	ARG	129	1.303	19.975	-0.790	1.00	24.39	1DIK1063
ATOM	972	O	ARG	129	0.612	19.448	-1.652	1.00	25.81	1DIK1064
ATOM	973	CB	ARG	129	1.673	22.351	-1.484	1.00	28.84	1DIK1065
ATOM	974	CG	ARG	129	3.139	22.218	-1.685	1.00	31.94	1DIK1066
ATOM	975	CD	ARG	129	3.536	23.072	-2.860	1.00	46.51	1DIK1067
ATOM	976	NE	ARG	129	4.899	22.774	-3.270	1.00	59.18	1DIK1068
ATOM	977	CZ	ARG	129	5.879	23.669	-3.295	1.00	67.18	1DIK1069
ATOM	978	NH1	ARG	129	5.643	24.936	-2.948	1.00	66.97	1DIK1070
ATOM	979	NH2	ARG	129	7.098	23.294	-3.672	1.00	69.63	1DIK1071
ATOM	980	N	ASN	130	2.266	19.306	-0.166	1.00	26.81	1DIK1072
ATOM	981	CA	ASN	130	2.456	17.883	-0.470	1.00	29.49	1DIK1073
ATOM	982	C	ASN	130	2.819	16.977	0.691	1.00	25.25	1DIK1074
ATOM	983	O	ASN	130	3.369	15.904	0.489	1.00	22.37	1DIK1075
ATOM	984	CB	ASN	130	3.407	17.643	-1.657	1.00	33.67	1DIK1076
ATOM	985	CG	ASN	130	4.679	18.415	-1.550	1.00	35.85	1DIK1077
ATOM	986	OD1	ASN	130	5.242	18.561	-0.472	1.00	41.17	1DIK1078
ATOM	997	ND2	ASN	130	5.148	18.926	-2.678	1.00	36.92	1DIK1079
ATOM	988	N	ILE	131	2.499	17.409	1.905	1.00	23.74	1DIK1080
ATOM	989	CA	ILE	131	2.729	16.600	3.087	1.00	22.76	1DIK1081
ATOM	990	C	ILE	131	1.405	16.555	3.857	1.00	22.22	1DIK1082
ATOM	991	O	ILE	131	0.706	17.568	3.994	1.00	20.81	1DIK1083
ATOM	992	CB	ILE	131	3.864	17.171	3.974	1.00	25.01	1DIK1084
ATOM	993	CG1	ILE	131	5.196	17.051	3.237	1.00	22.26	1DIK1085
ATOM	994	CG2	ILE	131	3.966	16.383	5.296	1.00	25.81	1DIK1086
ATOM	995	CD1	ILE	131	6.264	18.012	3.705	1.00	19.55	1DIK1087
ATOM	996	N	VAL	132	1.052	15.368	4.336	1.00	21.56	1DIK1088
ATOM	997	CA	VAL	132	-0.173	15.184	5.113	1.00	21.17	1DIK1089
ATOM	998	C	VAL	132	0.285	15.221	6.575	1.00	20.81	1DIK1090
ATOM	999	O	VAL	132	1.137	14.422	6.979	1.00	20.82	1DIK1091
ATOM	1000	CB	VAL	132	-0.841	13.807	4.803	1.00	18.52	1DIK1092
ATOM	1001	CG1	VAL	132	-2.123	13.651	5.597	1.00	14.56	1DIK1093
ATOM	1002	CG2	VAL	132	-1.126	13.686	3.320	1.00	13.43	1DIK1094
ATOM	1003	N	PRO	133	-0.260	16.151	7.383	1.00	20.75	1DIK1095
ATOM	1004	CA	PRO	133	0.116	16.273	8.798	1.00	17.17	1DIK1096
ATOM	1005	C	PRO	133	-0.288	15.036	9.585	1.00	20.37	1DIK1097
ATOM	1006	O	PRO	133	-1.268	14.364	9.229	1.00	19.54	1DIK1098
ATOM	1007	CB	PRO	133	-0.684	17.488	9.277	1.00	17.52	1DIK1099
ATOM	1008	CG	PRO	133	-1.029	18.231	8.029	1.00	19.74	1DIK1100
ATOM	1009	CD	PRO	133	-1.278	17.151	7.020	1.00	21.29	1DIK1101
ATOM	1010	N	PHE	134	0.467	14.721	10.641	1.00	20.95	1DIK1102
ATOM	1011	CA	PHE	134	0.131	13.596	11.514	1.00	18.61	1DIK1103
ATOM	1012	C	PHE	134	-0.583	14.285	12.677	1.00	17.69	1DIK1104
ATOM	1013	O	PHE	134	-0.016	15.175	13.310	1.00	17.93	1DIK1105
ATOM	1014	CB	PHE	134	1.368	12.847	12.003	1.00	17.50	1DIK1106
ATOM	1015	CG	PHE	134	1.040	11.715	12.941	1.00	17.28	1DIK1107
ATOM	1016	CD1	PHE	134	0.616	10.478	1			

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ATOM	1028	CD1	ILE	135	-4.731	16.360	11.245	1.00	11.33	1DIK1120
ATOM	1029	N	ARG	136	-3.074	14.259	16.335	1.00	13.24	1DIK1121
ATOM	1030	CA	ARG	136	-3.480	13.593	17.571	1.00	15.19	1DIK1122
ATOM	1031	C	ARG	136	-4.451	14.511	18.296	1.00	16.07	1DIK1123
ATOM	1032	O	ARG	136	-4.355	15.734	18.190	1.00	16.44	1DIK1124
ATOM	1033	CB	ARG	136	-2.289	13.322	18.487	1.00	13.97	1DIK1125
ATOM	1034	CG	ARG	136	-1.203	12.434	17.905	1.00	12.99	1DIK1126
ATOM	1035	CD	ARG	136	-0.176	12.079	18.973	1.00	14.14	1DIK1127
ATOM	1036	NE	ARG	136	0.441	13.277	19.540	1.00	22.30	1DIK1128
ATOM	1037	CZ	ARG	136	1.335	13.288	20.525	1.00	20.79	1DIK1129
ATOM	1038	NH1	ARG	136	1.743	12.150	21.081	1.00	17.01	1DIK1130
ATOM	1039	NH2	ARG	136	1.819	14.450	20.951	1.00	17.84	1DIK1131
ATOM	1040	N	SER	137	-5.378	13.918	19.035	1.00	16.59	1DIK1132
ATOM	1041	CA	SER	137	-6.381	14.663	19.789	1.00	14.27	1DIK1133
ATOM	1042	C	SER	137	-6.624	13.982	21.147	1.00	17.11	1DIK1134
ATOM	1043	O	SER	137	-6.549	12.754	21.272	1.00	16.51	1DIK1135
ATOM	1044	CB	SER	137	-7.682	14.703	18.966	1.00	13.24	1DIK1136
ATOM	1045	OG	SER	137	-8.804	15.178	19.690	1.00	13.55	1DIK1137
ATOM	1046	N	SER	138	-6.898	14.782	22.169	1.00	18.79	1DIK1138
ATOM	1047	CA	SER	138	-7.212	14.246	23.486	1.00	18.47	1DIK1139
ATOM	1048	C	SER	138	-8.651	13.714	23.338	1.00	20.67	1DIK1140
ATOM	1049	O	SER	138	-9.436	14.261	22.557	1.00	21.12	1DIK1141
ATOM	1050	CB	SER	138	-7.123	15.360	24.526	1.00	19.25	1DIK1142
ATOM	1051	OG	SER	138	-7.161	14.832	25.831	1.00	19.54	1DIK1143
ATOM	1052	N	GLY	139	-9.005	12.660	24.070	1.00	24.07	1DIK1144
ATOM	1053	CA	GLY	139	-10.326	12.064	23.923	1.00	23.86	1DIK1145
ATOM	1054	C	GLY	139	-11.511	12.774	24.550	1.00	26.14	1DIK1146
ATOM	1055	O	GLY	139	-12.114	12.261	25.491	1.00	33.68	1DIK1147
ATOM	1056	N	SER	140	-11.853	13.946	24.046	1.00	23.95	1DIK1148
ATOM	1057	CA	SER	140	-12.976	14.715	24.553	1.00	18.34	1DIK1149
ATOM	1058	C	SER	140	-13.709	15.148	23.296	1.00	21.76	1DIK1150
ATOM	1059	O	SER	140	-13.084	15.655	22.356	1.00	22.25	1DIK1151
ATOM	1060	CB	SER	140	-12.479	15.925	25.319	1.00	17.99	1DIK1152
ATOM	1061	OG	SER	140	-13.543	16.819	25.617	1.00	22.47	1DIK1153
ATOM	1062	N	SER	141	-15.024	14.959	23.274	1.00	19.07	1DIK1154
ATOM	1063	CA	SER	141	-15.825	15.278	22.097	1.00	21.60	1DIK1155
ATOM	1064	C	SER	141	-15.592	16.644	21.496	1.00	22.01	1DIK1156
ATOM	1065	O	SER	141	-15.468	16.764	20.275	1.00	23.16	1DIK1157
ATOM	1066	CB	SER	141	-17.303	15.111	22.399	1.00	23.43	1DIK1158
ATOM	1067	OG	SER	141	-17.480	14.054	23.319	1.00	40.45	1DIK1159
ATOM	1068	N	ARG	142	-15.526	17.675	22.335	1.00	19.81	1DIK1160
ATOM	1069	CA	ARG	142	-15.325	19.010	21.809	1.00	18.48	1DIK1161
ATOM	1070	C	ARG	142	-13.951	19.187	21.180	1.00	18.52	1DIK1162
ATOM	1071	O	ARG	142	-13.779	19.999	20.264	1.00	17.81	1DIK1163
ATOM	1072	CB	ARG	142	-15.580	20.072	22.885	1.00	17.69	1DIK1164
ATOM	1073	CG	ARG	142	-14.661	20.050	24.069	1.00	20.10	1DIK1165
ATOM	1074	CD	ARG	142	-14.952	21.269	24.913	1.00	23.72	1DIK1166
ATOM	1075	NE	ARG	142	-14.441	21.157	26.280	1.00	27.97	1DIK1167
ATOM	1076	CZ	ARG	142	-15.100	20.586	27.292	1.00	28.86	1DIK1168
ATOM	1077	NH1	ARG	142	-16.301	20.053	27.106	1.00	28.91	1DIK1169
ATOM	1078	NH2	ARG	142	-14.552	20.543	28.499	1.00	29.64	1DIK1170
ATOM	1079	N	VAL	143	-12.973	18.424	21.662	1.00	18.71	1DIK1171
ATOM	1080	CA	VAL	143	-11.620	18.516	21.137	1.00	16.09	1DIK1172
ATOM	1081	C	VAL	143	-11.561	17.777	19.799	1.00	19.00	1DIK1173
ATOM	1082	O	VAL	143	-11.031	18.303	18.802	1.00	19.96	1DIK1174
ATOM	1083	CB	VAL	143	-10.604	17.962	22.152	1.00	14.17	1DIK1175
ATOM	1084	CG1	VAL	143	-9.179	18.106	21.630	1.00	13.33	1DIK1176
ATOM	1085	CG2	VAL	143	-10.746	18.717	23.450	1.00	11.92	1DIK1177
ATOM	1086	N	ILE	144	-12.132	16.576	19.778	1.00	17.56	1DIK1178
ATOM	1087	CA	ILE	144	-12.177	15.752	18.582	1.00	17.36	1DIK1179
ATOM	1088	C	ILE	144	-12.882	16.490	17.431	1.00	19.27	1DIK1180
ATOM	1089	O	ILE	144	-12.400	16.492	16.281	1.00	20.66	1DIK1181
ATOM	1090	CB	ILE	144	-12.874	14.422	18.911	1.00	21.52	1DIK1182
ATOM	1091	CG1	ILE	144	-11.943	13.584	19.789	1.00	21.60	1DIK1183
ATOM	1092	CG2	ILE	144	-13.274	13.677	17.637	1.00	18.16	1DIK1184
ATOM	1093	CD1	ILE	144	-12.628	12.446	20.491	1.00	28.65	1DIK1185
ATOM	1094	N	ALA	145	-14.013	17.123	17.742	1.00	17.39	1DIK1186
ATOM	1095	CA	ALA	145	-14.780	17.889	16.752	1.00	15.97	1DIK1187
ATOM	1096	C	ALA	145	-13.951	19.066	16.243	1.00	18.18	1DIK1188
ATOM	1097	O	ALA	145	-14.049	19.436	15.073	1.00	20.54	1DIK1189
ATOM	1098	CB	ALA	145	-16.080	18.397	17.362	1.00	11.92	1DIK1190
ATOM	1099	N	SER	146	-13.141	19.654	17.125	1.00	17.49	1DIK1191
ATOM										

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ATOM	1113	CB	LYS	148	-13.422	16.821	12.631	1.00	20.50	1DIK1205
ATOM	1114	CG	LYS	148	-13.219	15.389	13.023	1.00	22.63	1DIK1206
ATOM	1115	CD	LYS	148	-14.539	14.722	13.227	1.00	27.17	1DIK1207
ATOM	1116	CE	LYS	148	-14.342	13.245	13.427	1.00	34.56	1DIK1208
ATOM	1117	NZ	LYS	148	-15.652	12.546	13.477	1.00	43.70	1DIK1209
ATOM	1118	N	LYS	149	-12.765	19.956	12.355	1.00	16.53	1DIK1210
ATOM	1119	CA	LYS	149	-13.049	21.221	11.680	1.00	19.05	1DIK1211
ATOM	1120	C	LYS	149	-11.756	21.821	11.132	1.00	19.26	1DIK1212
ATOM	1121	O	LYS	149	-11.747	22.412	10.050	1.00	19.18	1DIK1213
ATOM	1122	CB	LYS	149	-13.725	22.234	12.608	1.00	19.43	1DIK1214
ATOM	1123	CG	LYS	149	-15.018	21.775	13.196	1.00	25.49	1DIK1215
ATOM	1124	CD	LYS	149	-15.954	21.157	12.163	1.00	24.15	1DIK1216
ATOM	1125	CE	LYS	149	-16.677	22.178	11.350	1.00	24.54	1DIK1217
ATOM	1126	NZ	LYS	149	-17.717	21.492	10.530	1.00	23.29	1DIK1218
ATOM	1127	N	PHE	150	-10.672	21.677	11.885	1.00	17.03	1DIK1219
ATOM	1128	CA	PHE	150	-9.368	22.178	11.462	1.00	17.33	1DIK1220
ATOM	1129	C	PHE	150	-8.992	21.469	10.163	1.00	18.46	1DIK1221
ATOM	1130	O	PHE	150	-8.540	22.104	9.222	1.00	20.65	1DIK1222
ATOM	1131	CB	PHE	150	-8.321	21.892	12.555	1.00	17.32	1DIK1223
ATOM	1132	CG	PHE	150	-6.916	22.282	12.185	1.00	17.15	1DIK1224
ATOM	1133	CD1	PHE	150	-6.110	21.428	11.433	1.00	15.76	1DIK1225
ATOM	1134	CD2	PHE	150	-6.387	23.491	12.601	1.00	16.86	1DIK1226
ATOM	1135	CE1	PHE	150	-4.803	21.769	11.102	1.00	13.21	1DIK1227
ATOM	1136	CE2	PHE	150	-5.075	23.841	12.274	1.00	18.79	1DIK1228
ATOM	1137	CZ	PHE	150	-4.283	22.973	11.521	1.00	18.15	1DIK1229
ATOM	1138	N	ILE	151	-9.186	20.151	10.123	1.00	18.70	1DIK1230
ATOM	1139	CA	ILE	151	-8.887	19.337	8.949	1.00	16.84	1DIK1231
ATOM	1140	C	ILE	151	-9.700	19.829	7.751	1.00	21.25	1DIK1232
ATOM	1141	O	ILE	151	-9.212	19.895	6.621	1.00	22.35	1DIK1233
ATOM	1142	CB	ILE	151	-9.205	17.858	9.229	1.00	19.09	1DIK1234
ATOM	1143	CG1	ILE	151	-8.109	17.255	10.109	1.00	15.35	1DIK1235
ATOM	1144	CG2	ILE	151	-9.324	17.067	7.938	1.00	15.46	1DIK1236
ATOM	1145	CD1	ILE	151	-8.418	15.850	10.569	1.00	15.29	1DIK1237
ATOM	1146	N	GLU	152	-10.948	20.181	8.001	1.00	22.78	1DIK1238
ATOM	1147	CA	GLU	152	-11.821	20.692	6.954	1.00	22.06	1DIK1239
ATOM	1148	C	GLU	152	-11.208	21.958	6.339	1.00	22.51	1DIK1240
ATOM	1149	O	GLU	152	-11.019	22.033	5.125	1.00	27.84	1DIK1241
ATOM	1150	CB	GLU	152	-13.186	20.998	7.560	1.00	23.89	1DIK1242
ATOM	1151	CG	GLU	152	-14.321	21.169	6.578	1.00	27.41	1DIK1243
ATOM	1152	CD	GLU	152	-15.650	21.403	7.293	1.00	27.55	1DIK1244
ATOM	1153	OE1	GLU	152	-15.975	20.635	8.241	1.00	21.35	1DIK1245
ATOM	1154	OE2	GLU	152	-16.357	22.358	6.897	1.00	28.87	1DIK1246
ATOM	1155	N	GLY	153	-10.892	22.943	7.176	1.00	20.57	1DIK1247
ATOM	1156	CA	GLY	153	-10.305	24.177	6.693	1.00	19.76	1DIK1248
ATOM	1157	C	GLY	153	-8.990	23.965	5.955	1.00	23.46	1DIK1249
ATOM	1158	O	GLY	153	-8.773	24.528	4.886	1.00	25.73	1DIK1250
ATOM	1159	N	PHE	154	-8.114	23.145	6.528	1.00	22.50	1DIK1251
ATOM	1160	CA	PHE	154	-6.803	22.839	5.958	1.00	18.12	1DIK1252
ATOM	1161	C	PHE	154	-6.921	22.181	4.570	1.00	21.03	1DIK1253
ATOM	1162	O	PHE	154	-6.275	22.606	3.595	1.00	16.52	1DIK1254
ATOM	1163	CB	PHE	154	-6.048	21.909	6.937	1.00	16.95	1DIK1255
ATOM	1164	CG	PHE	154	-4.730	21.407	6.422	1.00	14.32	1DIK1256
ATOM	1165	CD1	PHE	154	-4.666	20.253	5.635	1.00	13.33	1DIK1257
ATOM	1166	CD2	PHE	154	-3.548	22.093	6.713	1.00	14.60	1DIK1258
ATOM	1167	CE1	PHE	154	-3.432	19.781	5.134	1.00	13.26	1DIK1259
ATOM	1168	CE2	PHE	154	-2.308	21.639	6.224	1.00	15.41	1DIK1260
ATOM	1169	CZ	PHE	154	-2.250	20.483	5.432	1.00	15.03	1DIK1261
ATOM	1170	N	GLN	155	-7.757	21.152	4.479	1.00	20.29	1DIK1262
ATOM	1171	CA	GLN	155	-7.921	20.441	3.231	1.00	21.66	1DIK1263
ATOM	1172	C	GLN	155	-8.626	21.290	2.170	1.00	25.36	1DIK1264
ATOM	1173	O	GLN	155	-8.255	21.256	0.983	1.00	26.48	1DIK1265
ATOM	1174	CB	GLN	155	-8.653	19.118	3.475	1.00	21.80	1DIK1266
ATOM	1175	CG	GLN	155	-8.471	18.085	2.369	1.00	27.70	1DIK1267
ATOM	1176	CD	GLN	155	-7.001	17.785	2.056	1.00	32.63	1DIK1268
ATOM	1177	OE1	GLN	155	-6.105	18.052	2.859	1.00	34.93	1DIK1269
ATOM	1178	NE2	GLN	155	-6.753	17.229	0.883	1.00	32.41	1DIK1270
ATOM	1179	N	SER	156	-9.628	22.059	2.581	1.00	22.38	1DIK1271
ATOM	1180	CA	SER	156	-10.355	22.911	1.632	1.00	27.24	1DIK1272
ATOM	1181	C	SER	156	-9.474	23.925	0.912	1.00	26.37	1DIK1273
ATOM	1182	O	SER	156	-9.733	24.273	-0.246	1.00	26.94	1DIK1274
ATOM	1183	CB	SER	156	-11.477	23.644	2.347	1.00	25.77	1DIK1275
ATOM	1184	OG	SER	156	-12.392	22.686	2.834	1.00	38.06	1DIK1276
ATOM	1185	N	THR							

Figure 8/16

ATOM	1198	CD	LYS	158	-3.200	19.556	0.829	1.00	24.06	1DIK1290
ATOM	1199	CE	LYS	158	-2.215	18.618	0.187	1.00	20.01	1DIK1291
ATOM	1200	N2	LYS	158	-1.529	17.800	1.220	1.00	21.14	1DIK1292
ATOM	1201	N	LEU	159	-7.151	21.972	-1.703	1.00	22.71	1DIK1293
ATOM	1202	CA	LEU	159	-7.819	21.638	-2.959	1.00	24.27	1DIK1294
ATOM	1203	C	LEU	159	-7.784	22.786	-3.940	1.00	26.47	1DIK1295
ATOM	1204	O	LEU	159	-7.781	22.558	-5.144	1.00	29.65	1DIK1296
ATOM	1205	CB	LEU	159	-9.286	21.297	-2.743	1.00	21.63	1DIK1297
ATOM	1206	CG	LEU	159	-9.611	20.081	-1.913	1.00	25.68	1DIK1298
ATOM	1207	CD1	LEU	159	-11.110	20.032	-1.750	1.00	29.97	1DIK1299
ATOM	1208	CD2	LEU	159	-9.069	18.832	-2.571	1.00	25.43	1DIK1300
ATOM	1209	N	LYS	160	-7.781	24.015	-3.428	1.00	27.67	1DIK1301
ATOM	1210	CA	LYS	160	-7.759	25.196	-4.281	1.00	27.18	1DIK1302
ATOM	1211	C	LYS	160	-6.343	25.615	-4.632	1.00	27.06	1DIK1303
ATOM	1212	O	LYS	160	-6.161	26.651	-5.268	1.00	31.28	1DIK1304
ATOM	1213	CB	LYS	160	-8.426	26.383	-3.592	1.00	29.62	1DIK1305
ATOM	1214	CG	LYS	160	-9.827	26.183	-3.080	1.00	31.58	1DIK1306
ATOM	1215	CD	LYS	160	-10.152	27.402	-2.228	1.00	41.75	1DIK1307
ATOM	1216	CE	LYS	160	-11.463	27.266	-1.482	1.00	49.39	1DIK1308
ATOM	1217	NZ	LYS	160	-11.817	28.556	-0.806	1.00	51.98	1DIK1309
ATOM	1218	N	ASP	161	-5.343	24.840	-4.223	1.00	25.13	1DIK1310
ATOM	1219	CA	ASP	161	-3.954	25.193	-4.506	1.00	27.83	1DIK1311
ATOM	1220	C	ASP	161	-3.416	24.467	-5.758	1.00	30.73	1DIK1312
ATOM	1221	O	ASP	161	-3.237	23.250	-5.753	1.00	29.13	1DIK1313
ATOM	1222	CB	ASP	161	-3.082	24.897	-3.276	1.00	27.42	1DIK1314
ATOM	1223	CG	ASP	161	-1.642	25.368	-3.442	1.00	30.76	1DIK1315
ATOM	1224	OD1	ASP	161	-1.314	25.998	-4.468	1.00	38.67	1DIK1316
ATOM	1225	OD2	ASP	161	-0.819	25.114	-2.542	1.00	29.87	1DIK1317
ATOM	1226	N	PRO	162	-3.134	25.222	-6.842	1.00	33.61	1DIK1318
ATOM	1227	CA	PRO	162	-2.622	24.685	-8.110	1.00	33.28	1DIK1319
ATOM	1228	C	PRO	162	-1.352	23.853	-7.960	1.00	33.91	1DIK1320
ATOM	1229	O	PRO	162	-1.148	22.886	-8.684	1.00	34.55	1DIK1321
ATOM	1230	CB	PRO	162	-2.354	25.947	-8.932	1.00	33.55	1DIK1322
ATOM	1231	CG	PRO	162	-3.370	26.919	-8.413	1.00	33.99	1DIK1323
ATOM	1232	CD	PRO	162	-3.274	26.690	-6.927	1.00	34.27	1DIK1324
ATOM	1233	N	ARG	163	-0.502	24.231	-7.017	1.00	36.00	1DIK1325
ATOM	1234	CA	ARG	163	0.758	23.529	-6.799	1.00	36.01	1DIK1326
ATOM	1235	C	ARG	163	0.664	22.345	-5.833	1.00	34.24	1DIK1327
ATOM	1236	O	ARG	163	1.669	21.693	-5.548	1.00	31.55	1DIK1328
ATOM	1237	CB	ARG	163	1.802	24.525	-6.310	1.00	42.55	1DIK1329
ATOM	1238	CG	ARG	163	1.929	25.753	-7.205	1.00	53.77	1DIK1330
ATOM	1239	CD	ARG	163	3.014	26.683	-6.704	1.00	63.94	1DIK1331
ATOM	1240	NE	ARG	163	4.304	25.997	-6.634	1.00	74.87	1DIK1332
ATOM	1241	C2	ARG	163	5.337	26.386	-5.886	1.00	79.93	1DIK1333
ATOM	1242	NH1	ARG	163	5.258	27.468	-5.123	1.00	82.39	1DIK1334
ATOM	1243	NH2	ARG	163	6.464	25.685	-5.902	1.00	84.40	1DIK1335
ATOM	1244	N	ALA	164	-0.539	22.072	-5.331	1.00	33.77	1DIK1336
ATOM	1245	CA	ALA	164	-0.762	20.962	-4.407	1.00	34.08	1DIK1337
ATOM	1246	C	ALA	164	-0.656	19.630	-5.149	1.00	35.29	1DIK1338
ATOM	1247	O	ALA	164	-0.984	19.540	-6.329	1.00	36.67	1DIK1339
ATOM	1248	CB	ALA	164	-2.130	21.087	-3.744	1.00	33.17	1DIK1340
ATOM	1249	N	GLN	165	-0.197	18.593	-4.460	1.00	38.92	1DIK1341
ATOM	1250	CA	GLN	165	-0.035	17.283	-5.076	1.00	38.56	1DIK1342
ATOM	1251	C	GLN	165	-1.336	16.530	-5.281	1.00	35.34	1DIK1343
ATOM	1252	O	GLN	165	-2.031	16.207	-4.319	1.00	38.47	1DIK1344
ATOM	1253	CB	GLN	165	0.895	16.422	-4.248	1.00	42.23	1DIK1345
ATOM	1254	CG	GLN	165	1.155	15.104	-4.907	1.00	52.03	1DIK1346
ATOM	1255	CD	GLN	165	2.472	14.565	-4.502	1.00	57.76	1DIK1347
ATOM	1256	OE1	GLN	165	3.461	14.718	-5.224	1.00	62.19	1DIK1348
ATOM	1257	NE2	GLN	165	2.516	13.932	-3.332	1.00	58.19	1DIK1349
ATOM	1258	N	PRO	166	-1.664	16.207	-6.542	1.00	33.99	1DIK1350
ATOM	1259	CA	PRO	166	-2.902	15.485	-6.886	1.00	31.51	1DIK1351
ATOM	1260	C	PRO	166	-3.006	14.057	-6.326	1.00	28.15	1DIK1352
ATOM	1261	O	PRO	166	-2.010	13.348	-6.240	1.00	30.43	1DIK1353
ATOM	1262	CB	PRO	166	-2.889	15.502	-8.420	1.00	28.29	1DIK1354
ATOM	1263	CG	PRO	166	-1.405	15.492	-8.737	1.00	29.54	1DIK1355
ATOM	1264	CD	PRO	166	-0.854	16.486	-7.747	1.00	28.70	1DIK1356
ATOM	1265	N	GLY	167	-4.215	13.656	-5.940	1.00	24.69	1DIK1357
ATOM	1266	CA	GLY	167	-4.453	12.313	-5.437	1.00	21.00	1DIK1358
ATOM	1267	C	GLY	167	-3.990	11.986	-4.032	1.00	25.28	1DIK1359
ATOM	1268	O	GLY	167	-4.190	10.867	-3.550	1.00	27.36	1DIK1360
ATOM	1269	N	GLN	168	-3.372	12.951	-3.367	1.00	24.69	1DIK1361
ATOM	1270	CA	GLN	168	-2.882	12.759	-2.010	1.00	24.46	1DIK1

Figure 8/17

ATOM	1283	OG	SER	169	-3.432	10.135	2.184	1.00	35.33	1DIK1375
ATOM	1284	N	SER	170	-6.418	12.724	2.444	1.00	25.08	1DIK1376
ATOM	1285	CA	SER	170	-6.756	13.759	3.414	1.00	23.05	1DIK1377
ATOM	1286	C	SER	170	-6.169	13.440	4.791	1.00	21.06	1DIK1378
ATOM	1287	O	SER	170	-5.867	12.280	5.101	1.00	19.23	1DIK1379
ATOM	1288	CB	SER	170	-8.273	13.838	3.586	1.00	20.90	1DIK1380
ATOM	1289	OG	SER	170	-8.909	14.154	2.380	1.00	31.58	1DIK1381
ATOM	1290	N	PRO	171	-5.993	14.463	5.637	1.00	20.40	1DIK1382
ATOM	1291	CA	PRO	171	-5.461	14.175	6.967	1.00	19.96	1DIK1383
ATOM	1292	C	PRO	171	-6.650	13.566	7.727	1.00	20.25	1DIK1384
ATOM	1293	O	PRO	171	-7.788	13.548	7.228	1.00	16.51	1DIK1385
ATOM	1294	CB	PRO	171	-5.147	15.566	7.531	1.00	22.09	1DIK1386
ATOM	1295	CG	PRO	171	-5.169	16.491	6.329	1.00	21.91	1DIK1387
ATOM	1296	CD	PRO	171	-6.236	15.905	5.471	1.00	22.51	1DIK1388
ATOM	1297	N	LYS	172	-6.397	13.076	8.931	1.00	20.67	1DIK1389
ATOM	1298	CA	LYS	172	-7.458	12.515	9.764	1.00	20.50	1DIK1390
ATOM	1299	C	LYS	172	-6.873	12.446	11.164	1.00	19.29	1DIK1391
ATOM	1300	O	LYS	172	-5.686	12.709	11.362	1.00	19.22	1DIK1392
ATOM	1301	CB	LYS	172	-7.867	11.114	9.286	1.00	18.29	1DIK1393
ATOM	1302	CG	LYS	172	-6.703	10.172	9.177	1.00	18.63	1DIK1394
ATOM	1303	CD	LYS	172	-7.122	8.761	9.350	1.00	23.30	1DIK1395
ATOM	1304	CE	LYS	172	-5.885	7.903	9.304	1.00	30.02	1DIK1396
ATOM	1305	NZ	LYS	172	-6.233	6.492	9.627	1.00	44.40	1DIK1397
ATOM	1306	N	ILE	173	-7.698	12.100	12.136	1.00	16.98	1DIK1398
ATOM	1307	CA	ILE	173	-7.218	11.998	13.493	1.00	19.06	1DIK1399
ATOM	1308	C	ILE	173	-6.583	10.614	13.635	1.00	22.40	1DIK1400
ATOM	1309	O	ILE	173	-7.266	9.593	13.768	1.00	21.26	1DIK1401
ATOM	1310	CB	ILE	173	-8.371	12.274	14.475	1.00	19.92	1DIK1402
ATOM	1311	CG1	ILE	173	-8.868	13.715	14.232	1.00	18.99	1DIK1403
ATOM	1312	CG2	ILE	173	-7.902	12.109	15.921	1.00	20.59	1DIK1404
ATOM	1313	CD1	ILE	173	-10.087	14.103	14.987	1.00	16.15	1DIK1405
ATOM	1314	N	ASP	174	-5.256	10.599	13.588	1.00	19.22	1DIK1406
ATOM	1315	CA	ASP	174	-4.504	9.366	13.667	1.00	18.78	1DIK1407
ATOM	1316	C	ASP	174	-4.495	8.689	15.021	1.00	20.21	1DIK1408
ATOM	1317	O	ASP	174	-4.507	7.463	15.087	1.00	23.44	1DIK1409
ATOM	1318	CB	ASP	174	-3.074	9.606	13.213	1.00	16.70	1DIK1410
ATOM	1319	CG	ASP	174	-3.001	10.130	11.793	1.00	21.97	1DIK1411
ATOM	1320	OD1	ASP	174	-3.185	9.320	10.853	1.00	28.66	1DIK1412
ATOM	1321	OD2	ASP	174	-2.763	11.348	11.618	1.00	15.14	1DIK1413
ATOM	1322	N	VAL	175	-4.464	9.470	16.099	1.00	19.64	1DIK1414
ATOM	1323	CA	VAL	175	-4.453	8.903	17.449	1.00	15.74	1DIK1415
ATOM	1324	C	VAL	175	-5.381	9.700	18.364	1.00	19.16	1DIK1416
ATOM	1325	O	VAL	175	-5.346	10.942	18.361	1.00	22.21	1DIK1417
ATOM	1326	CB	VAL	175	-3.016	8.940	18.088	1.00	15.96	1DIK1418
ATOM	1327	CG1	VAL	175	-3.013	8.205	19.427	1.00	11.79	1DIK1419
ATOM	1328	CG2	VAL	175	-1.967	8.323	17.154	1.00	15.25	1DIK1420
ATOM	1329	N	VAL	176	-6.220	9.009	19.135	1.00	16.60	1DIK1421
ATOM	1330	CA	VAL	176	-7.078	9.696	20.099	1.00	18.96	1DIK1422
ATOM	1331	C	VAL	176	-6.630	9.238	21.484	1.00	18.63	1DIK1423
ATOM	1332	O	VAL	176	-6.837	8.084	21.849	1.00	19.14	1DIK1424
ATOM	1333	CB	VAL	176	-8.585	9.390	19.923	1.00	19.70	1DIK1425
ATOM	1334	CG1	VAL	176	-9.382	10.058	21.050	1.00	18.39	1DIK1426
ATOM	1335	CG2	VAL	176	-9.071	9.919	18.580	1.00	17.14	1DIK1427
ATOM	1336	N	ILE	177	-6.017	10.135	22.249	1.00	16.49	1DIK1428
ATOM	1337	CA	ILE	177	-5.528	9.790	23.578	1.00	18.84	1DIK1429
ATOM	1338	C	ILE	177	-6.626	9.871	24.646	1.00	22.64	1DIK1430
ATOM	1339	O	ILE	177	-7.233	10.926	24.877	1.00	21.84	1DIK1431
ATOM	1340	CB	ILE	177	-4.331	10.669	23.959	1.00	17.93	1DIK1432
ATOM	1341	CG1	ILE	177	-3.258	10.548	22.876	1.00	21.31	1DIK1433
ATOM	1342	CG2	ILE	177	-3.747	10.209	25.293	1.00	13.33	1DIK1434
ATOM	1343	CD1	ILE	177	-2.129	11.530	23.031	1.00	24.99	1DIK1435
ATOM	1344	N	SER	178	-6.879	8.740	25.293	1.00	22.92	1DIK1436
ATOM	1345	CA	SER	178	-7.913	8.664	26.308	1.00	22.43	1DIK1437
ATOM	1346	C	SER	178	-7.692	9.620	27.469	1.00	23.70	1DIK1438
ATOM	1347	O	SER	178	-6.562	9.880	27.896	1.00	19.07	1DIK1439
ATOM	1348	CB	SER	178	-8.019	7.234	26.832	1.00	24.76	1DIK1440
ATOM	1349	OG	SER	178	-8.931	7.149	27.918	1.00	26.50	1DIK1441
ATOM	1350	N	GLU	179	-8.802	10.138	27.975	1.00	23.30	1DIK1442
ATOM	1351	CA	GLU	179	-8.763	11.032	29.109	1.00	24.10	1DIK1443
ATOM	1352	C	GLU	179	-9.145	10.299	30.390	1.00	26.08	1DIK1444
ATOM	1353	O	GLU	179	-9.372	10.930	31.424	1.00	28.11	1DIK1445
ATOM	1354	CB	GLU	179	-9.683	12.219	28.875	1.00	20.32	1DIK1446
ATOM	1355	CG	GLU	179	-9.046	13.277	28.013	1.00	19.78	1DI

Figure 8/18

ATOM	1368	CB	SER	181	-8.806	8.770	36.260	1.00	36.11	1DIK1460
ATOM	1369	OG	SER	181	-9.377	7.479	36.373	1.00	46.40	1DIK1461
ATOM	1370	N	SER	182	-6.798	6.821	34.500	1.00	27.14	1DIK1462
ATOM	1371	CA	SER	182	-5.615	5.963	34.488	1.00	29.83	1DIK1463
ATOM	1372	C	SER	182	-4.792	6.051	33.181	1.00	30.65	1DIK1464
ATOM	1373	O	SER	182	-3.808	5.329	33.013	1.00	35.32	1DIK1465
ATOM	1374	CB	SER	182	-6.023	4.496	34.726	1.00	32.11	1DIK1466
ATOM	1375	OG	SER	182	-6.967	4.032	33.757	1.00	33.33	1DIK1467
ATOM	1376	N	SER	183	-5.187	6.924	32.261	1.00	26.39	1DIK1468
ATOM	1377	CA	SER	183	-4.499	7.049	30.986	1.00	21.35	1DIK1469
ATOM	1378	C	SER	183	-3.268	7.953	30.986	1.00	18.80	1DIK1470
ATOM	1379	O	SER	183	-3.263	9.002	31.621	1.00	18.57	1DIK1471
ATOM	1380	CB	SER	183	-5.499	7.547	29.952	1.00	23.15	1DIK1472
ATOM	1381	OG	SER	183	-4.884	7.739	28.702	1.00	22.70	1DIK1473
ATOM	1382	N	ASN	184	-2.216	7.545	30.281	1.00	21.24	1DIK1474
ATOM	1383	CA	ASN	184	-1.012	8.383	30.160	1.00	22.85	1DIK1475
ATOM	1384	C	ASN	184	-1.287	9.264	28.942	1.00	22.55	1DIK1476
ATOM	1385	O	ASN	184	-1.275	8.786	27.805	1.00	21.64	1DIK1477
ATOM	1386	CB	ASN	184	0.233	7.542	29.918	1.00	25.23	1DIK1478
ATOM	1387	CG	ASN	184	0.476	6.547	31.027	1.00	29.76	1DIK1479
ATOM	1388	OD1	ASN	184	0.631	6.927	32.186	1.00	25.74	1DIK1480
ATOM	1389	ND2	ASN	184	0.505	5.259	30.680	1.00	31.61	1DIK1481
ATOM	1390	N	ASN	185	-1.536	10.546	29.197	1.00	20.70	1DIK1482
ATOM	1391	CA	ASN	185	-1.903	11.526	28.177	1.00	18.51	1DIK1483
ATOM	1392	C	ASN	185	-1.015	12.775	28.289	1.00	18.05	1DIK1484
ATOM	1393	O	ASN	185	-1.179	13.567	29.209	1.00	19.30	1DIK1485
ATOM	1394	CB	ASN	185	-3.386	11.879	28.421	1.00	17.92	1DIK1486
ATOM	1395	CG	ASN	185	-3.990	12.809	27.376	1.00	20.11	1DIK1487
ATOM	1396	OD1	ASN	185	-5.199	12.965	27.331	1.00	25.61	1DIK1488
ATOM	1397	ND2	ASN	185	-3.174	13.421	26.543	1.00	23.70	1DIK1489
ATOM	1398	N	THR	186	-0.089	12.962	27.350	1.00	18.02	1DIK1490
ATOM	1399	CA	THR	186	0.809	14.116	27.383	1.00	19.61	1DIK1491
ATOM	1400	C	THR	186	0.117	15.452	27.104	1.00	23.05	1DIK1492
ATOM	1401	O	THR	186	0.619	16.513	27.477	1.00	24.23	1DIK1493
ATOM	1402	CB	THR	186	1.959	13.971	26.367	1.00	20.27	1DIK1494
ATOM	1403	OG1	THR	186	1.410	13.772	25.062	1.00	19.57	1DIK1495
ATOM	1404	CG2	THR	186	2.871	12.815	26.731	1.00	15.78	1DIK1496
ATOM	1405	N	LEU	187	-1.030	15.398	26.443	1.00	22.21	1DIK1497
ATOM	1406	CA	LEU	187	-1.772	16.597	26.092	1.00	21.72	1DIK1498
ATOM	1407	C	LEU	187	-2.549	17.208	27.259	1.00	23.64	1DIK1499
ATOM	1408	O	LEU	187	-2.797	18.410	27.282	1.00	22.02	1DIK1500
ATOM	1409	CB	LEU	187	-2.716	16.276	24.933	1.00	23.09	1DIK1501
ATOM	1410	CG	LEU	187	-2.063	15.798	23.623	1.00	23.80	1DIK1502
ATOM	1411	CD1	LEU	187	-3.140	15.295	22.673	1.00	19.98	1DIK1503
ATOM	1412	CD2	LEU	187	-1.262	16.926	22.984	1.00	19.12	1DIK1504
ATOM	1413	N	ASP	188	-2.934	16.376	28.218	1.00	24.87	1DIK1505
ATOM	1414	CA	ASP	188	-3.684	16.815	29.399	1.00	28.75	1DIK1506
ATOM	1415	C	ASP	188	-3.540	15.688	30.424	1.00	27.51	1DIK1507
ATOM	1416	O	ASP	188	-4.431	14.851	30.584	1.00	30.17	1DIK1508
ATOM	1417	CB	ASP	188	-5.165	17.042	29.041	1.00	34.58	1DIK1509
ATOM	1418	CG	ASP	188	-5.958	17.724	30.171	1.00	41.42	1DIK1510
ATOM	1419	OD1	ASP	188	-5.474	18.727	30.765	1.00	42.84	1DIK1511
ATOM	1420	OD2	ASP	188	-7.079	17.246	30.461	1.00	42.36	1DIK1512
ATOM	1421	N	PRO	189	-2.398	15.653	31.129	1.00	26.10	1DIK1513
ATOM	1422	CA	PRO	189	-2.107	14.622	32.137	1.00	25.17	1DIK1514
ATOM	1423	C	PRO	189	-3.063	14.609	33.322	1.00	26.14	1DIK1515
ATOM	1424	O	PRO	189	-3.442	15.671	33.825	1.00	27.85	1DIK1516
ATOM	1425	CB	PRO	189	-0.677	14.959	32.579	1.00	21.04	1DIK1517
ATOM	1426	CG	PRO	189	-0.113	15.765	31.425	1.00	21.36	1DIK1518
ATOM	1427	CD	PRO	189	-1.286	16.615	31.026	1.00	22.23	1DIK1519
ATOM	1428	N	GLY	190	-3.442	13.413	33.766	1.00	24.92	1DIK1520
ATOM	1429	CA	GLY	190	-4.325	13.296	34.910	1.00	24.73	1DIK1521
ATOM	1430	C	GLY	190	-3.783	12.314	35.934	1.00	29.33	1DIK1522
ATOM	1431	O	GLY	190	-4.457	12.016	36.917	1.00	32.88	1DIK1523
ATOM	1432	N	THR	191	-2.563	11.824	35.722	1.00	26.97	1DIK1524
ATOM	1433	CA	THR	191	-1.964	10.826	36.603	1.00	26.69	1DIK1525
ATOM	1434	C	THR	191	-1.040	11.316	37.725	1.00	30.17	1DIK1526
ATOM	1435	O	THR	191	-0.535	10.507	38.518	1.00	32.24	1DIK1527
ATOM	1436	CB	THR	191	-1.202	9.781	35.776	1.00	25.25	1DIK1528
ATOM	1437	OG1	THR	191	-0.258	10.449	34.927	1.00	25.22	1DIK1529
ATOM	1438	CG2	THR	191	-2.170	8.967	34.918	1.00	24.37	1DIK1530
ATOM	1439	N	CYS	192	-0.805	12.621	37.800	1.00	29.82	1DIK1531
ATOM	1440	CA	CYS	192	0.055	13.164	38.847</td			

Figure 8/19

ATOM	1453	CA	VAL	194	-0.415	15.157	44.323	1.00	30.44	1DIK1545
ATOM	1454	C	VAL	194	-0.953	16.406	43.614	1.00	33.87	1DIK1546
ATOM	1455	O	VAL	194	-1.705	17.178	44.211	1.00	37.21	1DIK1547
ATOM	1456	CB	VAL	194	1.022	15.387	44.829	1.00	31.50	1DIK1548
ATOM	1457	CG1	VAL	194	1.175	16.793	45.390	1.00	27.45	1DIK1549
ATOM	1458	CG2	VAL	194	1.339	14.382	45.914	1.00	26.96	1DIK1550
ATOM	1459	N	PHE	195	-0.587	16.600	42.349	1.00	33.70	1DIK1551
ATOM	1460	CA	PHE	195	-1.049	17.768	41.598	1.00	32.23	1DIK1552
ATOM	1461	C	PHE	195	-2.575	17.802	41.485	1.00	33.46	1DIK1553
ATOM	1462	O	PHE	195	-3.195	18.853	41.665	1.00	34.15	1DIK1554
ATOM	1463	CB	PHE	195	-0.429	17.803	40.192	1.00	28.54	1DIK1555
ATOM	1464	CG	PHE	195	-0.987	18.890	39.311	1.00	24.30	1DIK1556
ATOM	1465	CD1	PHE	195	-0.563	20.207	39.457	1.00	21.84	1DIK1557
ATOM	1466	CD2	PHE	195	-1.952	18.595	38.344	1.00	22.84	1DIK1558
ATOM	1467	CE1	PHE	195	-1.087	21.237	38.650	1.00	28.26	1DIK1559
ATOM	1468	CE2	PHE	195	-2.486	19.610	37.529	1.00	26.40	1DIK1560
ATOM	1469	C2	PHE	195	-2.051	20.940	37.684	1.00	23.76	1DIK1561
ATOM	1470	N	GLU	196	-3.174	16.656	41.188	1.00	33.59	1DIK1562
ATOM	1471	CA	GLU	196	-4.618	16.574	41.048	1.00	34.08	1DIK1563
ATOM	1472	C	GLU	196	-5.357	16.966	42.328	1.00	35.44	1DIK1564
ATOM	1473	O	GLU	196	-6.497	17.411	42.266	1.00	35.61	1DIK1565
ATOM	1474	CB	GLU	196	-5.026	15.165	40.602	1.00	34.98	1DIK1566
ATOM	1475	CG	GLU	196	-4.509	14.774	39.211	1.00	37.27	1DIK1567
ATOM	1476	CD	GLU	196	-5.098	15.638	38.094	1.00	40.35	1DIK1568
ATOM	1477	OE1	GLU	196	-6.338	15.806	38.053	1.00	45.20	1DIK1569
ATOM	1478	OE2	GLU	196	-4.332	16.154	37.256	1.00	33.72	1DIK1570
ATOM	1479	N	ASP	197	-4.715	16.807	43.483	1.00	38.29	1DIK1571
ATOM	1480	CA	ASP	197	-5.352	17.160	44.758	1.00	40.02	1DIK1572
ATOM	1481	C	ASP	197	-5.141	18.621	45.173	1.00	38.28	1DIK1573
ATOM	1482	O	ASP	197	-5.770	19.093	46.110	1.00	38.49	1DIK1574
ATOM	1483	CB	ASP	197	-4.862	16.234	45.887	1.00	43.17	1DIK1575
ATOM	1484	CG	ASP	197	-5.402	14.805	45.766	1.00	48.76	1DIK1576
ATOM	1485	OD1	ASP	197	-6.582	14.630	45.373	1.00	50.32	1DIK1577
ATOM	1486	OD2	ASP	197	-4.640	13.853	46.069	1.00	49.19	1DIK1578
ATOM	1487	N	SER	198	-4.261	19.327	44.470	1.00	38.44	1DIK1579
ATOM	1488	CA	SER	198	-3.928	20.724	44.763	1.00	38.19	1DIK1580
ATOM	1489	C	SER	198	-5.131	21.675	44.824	1.00	39.35	1DIK1581
ATOM	1490	O	SER	198	-6.001	21.639	43.952	1.00	38.20	1DIK1582
ATOM	1491	CB	SER	198	-2.929	21.231	43.713	1.00	34.00	1DIK1583
ATOM	1492	OG	SER	198	-2.404	22.508	44.049	1.00	37.33	1DIK1584
ATOM	1493	N	GLU	199	-5.175	22.530	45.848	1.00	40.37	1DIK1585
ATOM	1494	CA	GLU	199	-6.262	23.505	45.981	1.00	42.79	1DIK1586
ATOM	1495	C	GLU	199	-5.735	24.932	45.904	1.00	41.90	1DIK1587
ATOM	1496	O	GLU	199	-6.453	25.886	46.228	1.00	41.14	1DIK1588
ATOM	1497	CB	GLU	199	-7.010	23.322	47.295	1.00	47.81	1DIK1589
ATOM	1498	CG	GLU	199	-7.935	22.127	47.334	1.00	56.13	1DIK1590
ATOM	1499	CD	GLU	199	-8.400	21.817	48.752	1.00	62.12	1DIK1591
ATOM	1500	OE1	GLU	199	-7.533	21.713	49.663	1.00	60.51	1DIK1592
ATOM	1501	OE2	GLU	199	-9.631	21.680	48.952	1.00	64.72	1DIK1593
ATOM	1502	N	LEU	200	-4.485	25.079	45.465	1.00	39.80	1DIK1594
ATOM	1503	CA	LEU	200	-3.861	26.391	45.356	1.00	38.33	1DIK1595
ATOM	1504	C	LEU	200	-4.700	27.405	44.565	1.00	40.30	1DIK1596
ATOM	1505	O	LEU	200	-4.924	28.526	45.027	1.00	41.57	1DIK1597
ATOM	1506	CB	LEU	200	-2.469	26.260	44.740	1.00	34.44	1DIK1598
ATOM	1507	CG	LEU	200	-1.659	27.564	44.728	1.00	38.04	1DIK1599
ATOM	1508	CD1	LEU	200	-1.503	28.104	46.144	1.00	29.88	1DIK1600
ATOM	1509	CD2	LEU	200	-0.297	27.334	44.087	1.00	36.27	1DIK1601
ATOM	1510	N	ALA	201	-5.170	27.012	43.384	1.00	39.72	1DIK1602
ATOM	1511	CA	ALA	201	-5.974	27.901	42.549	1.00	38.07	1DIK1603
ATOM	1512	C	ALA	201	-7.230	28.400	43.247	1.00	39.57	1DIK1604
ATOM	1513	O	ALA	201	-7.623	29.541	43.048	1.00	41.56	1DIK1605
ATOM	1514	CB	ALA	201	-6.354	27.211	41.249	1.00	33.45	1DIK1606
ATOM	1515	N	ASP	202	-7.863	27.557	44.060	1.00	42.79	1DIK1607
ATOM	1516	CA	ASP	202	-9.089	27.949	44.767	1.00	46.09	1DIK1608
ATOM	1517	C	ASP	202	-8.812	29.026	45.804	1.00	46.30	1DIK1609
ATOM	1518	O	ASP	202	-9.596	29.968	45.962	1.00	48.14	1DIK1610
ATOM	1519	CB	ASP	202	-9.719	26.748	45.461	1.00	52.71	1DIK1611
ATOM	1520	CG	ASP	202	-10.027	25.624	44.503	1.00	62.26	1DIK1612
ATOM	1521	OD1	ASP	202	-10.673	25.892	43.457	1.00	62.64	1DIK1613
ATOM	1522	OD2	ASP	202	-9.617	24.476	44.804	1.00	68.25	1DIK1614
ATOM	1523	N	THR	203	-7.693	28.875	46.507	1.00	42.43	1DIK1615
ATOM	1524	CA	THR	203	-7.283	29.828	47.524	1.00	40.28	1DIK1616
ATOM	1525	C								

Figure 8/20

ATOM	1538	CA	GLU	205	-9.343	32.778	43.331	1.00	36.22	1DIK1630
ATOM	1539	C	GLU	205	-10.125	33.501	44.414	1.00	36.92	1DIK1631
ATOM	1540	O	GLU	205	-10.662	34.580	44.182	1.00	40.62	1DIK1632
ATOM	1541	CB	GLU	205	-10.201	31.655	42.750	1.00	33.02	1DIK1633
ATOM	1542	CG	GLU	205	-11.607	32.094	42.365	1.00	39.52	1DIK1634
ATOM	1543	CD	GLU	205	-12.312	31.094	41.454	1.00	46.03	1DIK1635
ATOM	1544	OE1	GLU	205	-12.076	29.875	41.597	1.00	48.84	1DIK1636
ATOM	1545	OE2	GLU	205	-13.105	31.526	40.585	1.00	53.38	1DIK1637
ATOM	1546	N	ALA	206	-10.179	32.897	45.597	1.00	39.03	1DIK1638
ATOM	1547	CA	ALA	206	-10.898	33.464	46.731	1.00	37.04	1DIK1639
ATOM	1548	C	ALA	206	-10.262	34.787	47.160	1.00	36.03	1DIK1640
ATOM	1549	O	ALA	206	-10.954	35.803	47.316	1.00	32.23	1DIK1641
ATOM	1550	CB	ALA	206	-10.909	32.472	47.891	1.00	32.31	1DIK1642
ATOM	1551	N	ASN	207	-8.946	34.774	47.335	1.00	35.44	1DIK1643
ATOM	1552	CA	ASN	207	-8.231	35.971	47.754	1.00	40.04	1DIK1644
ATOM	1553	C	ASN	207	-8.484	37.150	46.836	1.00	39.71	1DIK1645
ATOM	1554	O	ASN	207	-8.838	38.235	47.307	1.00	42.35	1DIK1646
ATOM	1555	CB	ASN	207	-6.716	35.722	47.841	1.00	43.98	1DIK1647
ATOM	1556	CG	ASN	207	-6.331	34.791	48.992	1.00	48.43	1DIK1648
ATOM	1557	OD1	ASN	207	-7.115	34.557	49.922	1.00	46.90	1DIK1649
ATOM	1558	ND2	ASN	207	-5.111	34.252	48.930	1.00	50.65	1DIK1650
ATOM	1559	N	PHE	208	-8.318	36.946	45.531	1.00	37.95	1DIK1651
ATOM	1560	CA	PHE	208	-8.499	38.044	44.591	1.00	34.08	1DIK1652
ATOM	1561	C	PHE	208	-9.925	38.528	44.400	1.00	32.61	1DIK1653
ATOM	1562	O	PHE	208	-10.156	39.739	44.401	1.00	32.67	1DIK1654
ATOM	1563	CB	PHE	208	-7.878	37.726	43.229	1.00	32.46	1DIK1655
ATOM	1564	CG	PHE	208	-7.841	38.915	42.287	1.00	32.48	1DIK1656
ATOM	1565	CD1	PHE	208	-6.951	39.966	42.506	1.00	30.74	1DIK1657
ATOM	1566	CD2	PHE	208	-8.713	38.991	41.193	1.00	28.48	1DIK1658
ATOM	1567	CE1	PHE	208	-6.929	41.081	41.650	1.00	29.80	1DIK1659
ATOM	1568	CE2	PHE	208	-8.700	40.090	40.339	1.00	26.94	1DIK1660
ATOM	1569	CZ	PHE	208	-7.805	41.140	40.568	1.00	30.80	1DIK1661
ATOM	1570	N	THR	209	-10.887	37.620	44.238	1.00	31.39	1DIK1662
ATOM	1571	CA	THR	209	-12.259	38.074	44.026	1.00	33.60	1DIK1663
ATOM	1572	C	THR	209	-12.678	38.987	45.171	1.00	34.71	1DIK1664
ATOM	1573	O	THR	209	-13.415	39.954	44.963	1.00	36.94	1DIK1665
ATOM	1574	CB	THR	209	-13.280	36.904	43.844	1.00	32.70	1DIK1666
ATOM	1575	OG1	THR	209	-13.295	36.072	45.004	1.00	36.54	1DIK1667
ATOM	1576	CG2	THR	209	-12.919	36.057	42.631	1.00	31.98	1DIK1668
ATOM	1577	N	ALA	210	-12.193	38.693	46.376	1.00	37.10	1DIK1669
ATOM	1578	CA	ALA	210	-12.504	39.505	47.557	1.00	37.69	1DIK1670
ATOM	1579	C	ALA	210	-12.126	40.977	47.342	1.00	39.15	1DIK1671
ATOM	1580	O	ALA	210	-12.801	41.876	47.849	1.00	42.92	1DIK1672
ATOM	1581	CB	ALA	210	-11.781	38.954	48.770	1.00	31.71	1DIK1673
ATOM	1582	N	THR	211	-11.067	41.222	46.576	1.00	36.88	1DIK1674
ATOM	1583	CA	THR	211	-10.610	42.581	46.310	1.00	36.47	1DIK1675
ATOM	1584	C	THR	211	-11.462	43.431	45.341	1.00	35.57	1DIK1676
ATOM	1585	O	THR	211	-11.188	44.629	45.192	1.00	37.01	1DIK1677
ATOM	1586	CB	THR	211	-9.170	42.383	45.769	1.00	37.77	1DIK1678
ATOM	1587	OG1	THR	211	-9.190	42.206	44.388	1.00	40.97	1DIK1679
ATOM	1588	CG2	THR	211	-8.297	41.590	46.537	1.00	35.34	1DIK1680
ATOM	1589	N	PHE	212	-12.473	42.858	44.683	1.00	29.14	1DIK1681
ATOM	1590	CA	PHE	212	-13.280	43.659	43.749	1.00	24.90	1DIK1682
ATOM	1591	C	PHE	212	-14.736	41.224	43.559	1.00	27.12	1DIK1683
ATOM	1592	O	PHE	212	-15.577	44.041	43.190	1.00	31.27	1DIK1684
ATOM	1593	CB	PHE	212	-12.583	43.755	42.371	1.00	25.16	1DIK1685
ATOM	1594	CG	PHE	212	-12.772	42.534	41.491	1.00	26.99	1DIK1686
ATOM	1595	CD1	PHE	212	-12.017	41.382	41.689	1.00	24.61	1DIK1687
ATOM	1596	CD2	PHE	212	-13.724	42.538	40.469	1.00	29.36	1DIK1688
ATOM	1597	CE1	PHE	212	-12.213	40.252	40.883	1.00	26.98	1DIK1689
ATOM	1598	CE2	PHE	212	-13.926	41.417	39.661	1.00	23.41	1DIK1690
ATOM	1599	CZ	PHE	212	-13.170	40.273	39.869	1.00	24.28	1DIK1691
ATOM	1600	N	VAL	213	-15.045	41.954	43.798	1.00	26.22	1DIK1692
ATOM	1601	CA	VAL	213	-16.414	41.458	43.637	1.00	26.85	1DIK1693
ATOM	1602	C	VAL	213	-17.424	41.996	44.676	1.00	31.61	1DIK1694
ATOM	1603	O	VAL	213	-18.554	42.341	44.322	1.00	30.84	1DIK1695
ATOM	1604	CB	VAL	213	-16.449	39.905	43.611	1.00	22.75	1DIK1696
ATOM	1605	CG1	VAL	213	-17.854	39.405	43.418	1.00	16.76	1DIK1697
ATOM	1606	CG2	VAL	213	-15.592	39.403	42.489	1.00	20.78	1DIK1698
ATOM	1607	N	PRO	214	-17.041	42.076	45.966	1.00	33.45	1DIK1699
ATOM	1608	CA	PRO	214	-17.969	42.585	46.989	1.00	33.40	1DIK1700
ATOM	1609	C	PRO	214	-18.707	43.889	46.624	1.00	31.74	1DIK

Figure 8/21

ATOM	1623	O	ILE	216	-22.578	44.429	42.734	1.00	28.40	1DIK1715
ATOM	1624	CB	ILE	216	-19.532	43.797	41.512	1.00	24.43	1DIK1716
ATOM	1625	CG1	ILE	216	-18.194	44.372	41.032	1.00	25.18	1DIK1717
ATOM	1626	CG2	ILE	216	-20.446	43.596	40.334	1.00	24.08	1DIK1718
ATOM	1627	CD1	ILE	216	-17.423	43.463	40.073	1.00	19.59	1DIK1719
ATOM	1628	N	ARG	217	-21.231	43.136	44.016	1.00	32.27	1DIK1720
ATOM	1629	CA	ARG	217	-22.326	42.415	44.661	1.00	33.05	1DIK1721
ATOM	1630	C	ARG	217	-23.283	43.390	45.348	1.00	34.41	1DIK1722
ATOM	1631	O	ARG	217	-24.508	43.263	45.220	1.00	34.77	1DIK1723
ATOM	1632	CB	ARG	217	-21.798	41.415	45.689	1.00	32.26	1DIK1724
ATOM	1633	CG	ARG	217	-22.910	40.737	46.468	1.00	28.72	1DIK1725
ATOM	1634	CD	ARG	217	-22.379	39.772	47.495	1.00	33.69	1DIK1726
ATOM	1635	NE	ARG	217	-21.418	40.352	48.438	1.00	37.21	1DIK1727
ATOM	1636	CZ	ARG	217	-21.677	41.336	49.303	1.00	38.84	1DIK1728
ATOM	1637	NH1	ARG	217	-22.879	41.908	49.355	1.00	34.37	1DIK1729
ATOM	1638	NH2	ARG	217	-20.713	41.754	50.120	1.00	35.90	1DIK1730
ATOM	1639	N	GLN	218	-22.729	44.359	46.073	1.00	32.95	1DIK1731
ATOM	1640	CA	GLN	218	-23.562	45.352	46.749	1.00	36.19	1DIK1732
ATOM	1641	C	GLN	218	-24.392	46.172	45.763	1.00	36.45	1DIK1733
ATOM	1642	O	GLN	218	-25.565	46.450	46.026	1.00	36.62	1DIK1734
ATOM	1643	CB	GLN	218	-22.715	46.275	47.617	1.00	37.01	1DIK1735
ATOM	1644	CG	GLN	218	-22.118	45.574	48.819	1.00	42.03	1DIK1736
ATOM	1645	CD	GLN	218	-21.371	46.519	49.727	1.00	44.82	1DIK1737
ATOM	1646	OE1	GLN	218	-21.019	47.631	49.335	1.00	47.97	1DIK1738
ATOM	1647	NE2	GLN	218	-21.123	46.083	50.955	1.00	49.64	1DIK1739
ATOM	1648	N	ARG	219	-23.799	46.548	44.629	1.00	34.39	1DIK1740
ATOM	1649	CA	ARG	219	-24.529	47.313	43.624	1.00	31.62	1DIK1741
ATOM	1650	C	ARG	219	-25.691	46.487	43.091	1.00	33.49	1DIK1742
ATOM	1651	O	ARG	219	-26.813	46.984	42.982	1.00	34.34	1DIK1743
ATOM	1652	CB	ARG	219	-23.618	47.722	42.470	1.00	29.81	1DIK1744
ATOM	1653	CG	ARG	219	-24.290	48.626	41.446	1.00	27.77	1DIK1745
ATOM	1654	CD	ARG	219	-23.291	49.121	40.410	1.00	28.23	1DIK1746
ATOM	1655	NE	ARG	219	-22.904	48.071	39.462	1.00	27.67	1DIK1747
ATOM	1656	CZ	ARG	219	-21.656	47.650	39.254	1.00	29.17	1DIK1748
ATOM	1657	NH1	ARG	219	-20.638	48.169	39.933	1.00	21.50	1DIK1749
ATOM	1658	NH2	ARG	219	-21.423	46.698	38.360	1.00	32.18	1DIK1750
ATOM	1659	N	LEU	220	-25.437	45.223	42.765	1.00	32.50	1DIK1751
ATOM	1660	CA	LEU	220	-26.504	44.377	42.243	1.00	33.49	1DIK1752
ATOM	1661	C	LEU	220	-27.609	44.104	43.260	1.00	32.41	1DIK1753
ATOM	1662	O	LEU	220	-28.790	44.123	42.901	1.00	29.58	1DIK1754
ATOM	1663	CB	LEU	220	-25.948	43.043	41.727	1.00	34.41	1DIK1755
ATOM	1664	CG	LEU	220	-25.043	43.081	40.494	1.00	36.51	1DIK1756
ATOM	1665	CD1	LEU	220	-24.636	41.657	40.138	1.00	35.97	1DIK1757
ATOM	1666	CD2	LEU	220	-25.758	43.753	39.331	1.00	27.80	1DIK1758
ATOM	1667	N	GLU	221	-27.233	43.848	44.517	1.00	35.98	1DIK1759
ATOM	1668	CA	GLU	221	-28.213	43.560	45.576	1.00	38.20	1DIK1760
ATOM	1669	C	GLU	221	-29.100	44.771	45.795	1.00	39.87	1DIK1761
ATOM	1670	O	GLU	221	-30.302	44.646	46.042	1.00	40.20	1DIK1762
ATOM	1671	CB	GLU	221	-27.519	43.179	46.881	1.00	35.73	1DIK1763
ATOM	1672	CG	GLU	221	-26.800	41.848	46.816	1.00	39.22	1DIK1764
ATOM	1673	CD	GLU	221	-26.340	41.346	48.176	1.00	42.91	1DIK1765
ATOM	1674	OE1	GLU	221	-25.555	42.054	48.861	1.00	43.49	1DIK1766
ATOM	1675	OE2	GLU	221	-26.770	40.234	48.557	1.00	41.59	1DIK1767
ATOM	1676	N	ASN	222	-28.486	45.943	45.689	1.00	41.49	1DIK1768
ATOM	1677	CA	ASN	222	-29.182	47.208	45.841	1.00	45.54	1DIK1769
ATOM	1678	C	ASN	222	-30.139	47.515	44.672	1.00	43.33	1DIK1770
ATOM	1679	O	ASN	222	-31.257	47.971	44.903	1.00	45.33	1DIK1771
ATOM	1680	CB	ASN	222	-28.158	48.329	46.017	1.00	54.00	1DIK1772
ATOM	1681	CG	ASN	222	-28.797	49.701	46.091	1.00	62.65	1DIK1773
ATOM	1682	OD1	ASN	222	-28.256	50.675	45.558	1.00	68.49	1DIK1774
ATOM	1683	ND2	ASN	222	-29.951	49.793	46.752	1.00	66.30	1DIK1775
ATOM	1684	N	ASP	223	-29.715	47.268	43.433	1.00	41.09	1DIK1776
ATOM	1685	CA	ASP	223	-30.562	47.521	42.256	1.00	37.20	1DIK1777
ATOM	1686	C	ASP	223	-31.655	46.482	42.022	1.00	38.11	1DIK1778
ATOM	1687	O	ASP	223	-32.712	46.809	41.482	1.00	39.42	1DIK1779
ATOM	1688	CB	ASP	223	-29.717	47.636	40.990	1.00	35.50	1DIK1780
ATOM	1689	CG	ASP	223	-28.772	48.821	41.817	1.00	38.50	1DIK1781
ATOM	1690	OD1	ASP	223	-28.977	49.753	41.826	1.00	40.58	1DIK1782
ATOM	1691	OD2	ASP	223	-27.811	48.827	40.220	1.00	41.14	1DIK1783
ATOM	1692	N	LEU	224	-31.412	45.231	42.405	1.00	40.35	1DIK1784
ATOM	1693	CA	LEU	224	-32.427	44.188	42.232	1.00	45.31	1DIK1785
ATOM	1694	C	LEU	224	-32.971					

Figure 8/22

ATOM	1708	C	GLY	226	-34.226	40.060	46.731	1.00	44.37	1DIK1800
ATOM	1709	O	GLY	226	-34.461	38.900	47.051	1.00	47.89	1DIK1801
ATOM	1710	N	VAL	227	-33.119	40.422	46.108	1.00	42.94	1DIK1802
ATOM	1711	CA	VAL	227	-32.108	39.465	45.727	1.00	43.07	1DIK1803
ATOM	1712	C	VAL	227	-30.903	39.493	46.670	1.00	41.79	1DIK1804
ATOM	1713	O	VAL	227	-30.485	40.560	47.135	1.00	41.57	1DIK1805
ATOM	1714	CB	VAL	227	-31.676	39.750	44.252	1.00	45.33	1DIK1806
ATOM	1715	CG1	VAL	227	-30.316	39.167	43.947	1.00	44.28	1DIK1807
ATOM	1716	CG2	VAL	227	-32.721	39.189	43.297	1.00	44.62	1DIK1808
ATOM	1717	N	THR	228	-30.371	38.307	46.963	1.00	40.83	1DIK1809
ATOM	1718	CA	THR	228	-29.166	38.159	47.785	1.00	39.67	1DIK1810
ATOM	1719	C	THR	228	-28.234	37.336	46.893	1.00	37.22	1DIK1811
ATOM	1720	O	THR	228	-28.679	36.394	46.235	1.00	33.46	1DIK1812
ATOM	1721	CB	THR	228	-29.412	37.398	49.124	1.00	41.63	1DIK1813
ATOM	1722	OG1	THR	228	-29.990	36.116	48.867	1.00	44.83	1DIK1814
ATOM	1723	CG2	THR	228	-30.339	38.177	50.021	1.00	43.36	1DIK1815
ATOM	1724	N	LEU	229	-26.957	37.689	46.862	1.00	36.42	1DIK1816
ATOM	1725	CA	LEU	229	-25.991	36.988	46.022	1.00	35.85	1DIK1817
ATOM	1726	C	LEU	229	-24.689	36.735	46.771	1.00	36.00	1DIK1818
ATOM	1727	O	LEU	229	-24.302	37.520	47.630	1.00	37.29	1DIK1819
ATOM	1728	CB	LEU	229	-25.664	37.848	44.799	1.00	35.69	1DIK1820
ATOM	1729	CG	LEU	229	-26.790	38.240	43.850	1.00	31.77	1DIK1821
ATOM	1730	CD1	LEU	229	-26.254	39.233	42.860	1.00	32.31	1DIK1822
ATOM	1731	CD2	LEU	229	-27.334	37.014	43.143	1.00	31.68	1DIK1823
ATOM	1732	N	THR	230	-24.011	35.643	46.447	1.00	33.91	1DIK1824
ATOM	1733	CA	THR	230	-22.729	35.359	47.072	1.00	34.10	1DIK1825
ATOM	1734	C	THR	230	-21.743	35.959	46.083	1.00	34.69	1DIK1826
ATOM	1735	O	THR	230	-22.119	36.265	44.944	1.00	32.68	1DIK1827
ATOM	1736	CB	THR	230	-22.466	33.838	47.178	1.00	34.26	1DIK1828
ATOM	1737	OG1	THR	230	-22.463	33.260	45.870	1.00	30.93	1DIK1829
ATOM	1738	CG2	THR	230	-23.552	33.151	47.997	1.00	31.47	1DIK1830
ATOM	1739	N	ASP	231	-20.493	36.131	46.494	1.00	37.66	1DIK1831
ATOM	1740	CA	ASP	231	-19.478	36.674	45.592	1.00	39.60	1DIK1832
ATOM	1741	C	ASP	231	-19.312	35.794	44.344	1.00	40.76	1DIK1833
ATOM	1742	O	ASP	231	-19.186	36.303	43.227	1.00	43.31	1DIK1834
ATOM	1743	CB	ASP	231	-18.138	36.827	46.313	1.00	39.61	1DIK1835
ATOM	1744	CG	ASP	231	-18.147	37.956	47.321	1.00	44.99	1DIK1836
ATOM	1745	OD1	ASP	231	-19.042	38.825	47.233	1.00	45.50	1DIK1837
ATOM	1746	OD2	ASP	231	-17.254	37.976	48.202	1.00	49.54	1DIK1838
ATOM	1747	N	THR	232	-19.324	34.479	44.544	1.00	38.28	1DIK1839
ATOM	1748	CA	THR	232	-19.188	33.520	43.458	1.00	34.10	1DIK1840
ATOM	1749	C	THR	232	-20.280	33.679	42.416	1.00	32.21	1DIK1841
ATOM	1750	O	THR	232	-19.994	33.663	41.222	1.00	34.55	1DIK1842
ATOM	1751	CB	THR	232	-19.210	32.075	44.010	1.00	34.37	1DIK1843
ATOM	1752	OG1	THR	232	-18.074	31.896	44.856	1.00	35.55	1DIK1844
ATOM	1753	CG2	THR	232	-19.163	31.037	42.894	1.00	26.21	1DIK1845
ATOM	1754	N	GLU	233	-21.525	33.835	42.856	1.00	28.27	1DIK1846
ATOM	1755	CA	GLU	233	-22.637	33.978	41.919	1.00	29.61	1DIK1847
ATOM	1756	C	GLU	233	-22.500	35.196	41.016	1.00	27.81	1DIK1848
ATOM	1757	O	GLU	233	-22.923	35.162	39.872	1.00	30.27	1DIK1849
ATOM	1758	CB	GLU	233	-23.970	34.029	42.660	1.00	32.29	1DIK1850
ATOM	1759	CG	GLU	233	-24.262	32.784	43.483	1.00	38.65	1DIK1851
ATOM	1760	CD	GLU	233	-25.539	32.893	44.298	1.00	41.41	1DIK1852
ATOM	1761	OE1	GLU	233	-25.716	33.897	45.041	1.00	39.47	1DIK1853
ATOM	1762	OE2	GLU	233	-26.366	31.961	44.188	1.00	43.44	1DIK1854
ATOM	1763	N	VAL	234	-21.916	36.270	41.529	1.00	26.78	1DIK1855
ATOM	1764	CA	VAL	234	-21.718	37.471	40.730	1.00	27.81	1DIK1856
ATOM	1765	C	VAL	234	-20.779	37.131	39.555	1.00	28.07	1DIK1857
ATOM	1766	O	VAL	234	-21.031	37.532	38.409	1.00	27.61	1DIK1858
ATOM	1767	CB	VAL	234	-21.139	38.631	41.599	1.00	29.25	1DIK1859
ATOM	1768	CG1	VAL	234	-20.669	39.790	40.719	1.00	26.00	1DIK1860
ATOM	1769	CG2	VAL	234	-22.202	39.114	42.574	1.00	23.62	1DIK1861
ATOM	1770	N	THR	235	-19.712	36.383	39.830	1.00	25.71	1DIK1862
ATOM	1771	CA	THR	235	-18.784	35.991	38.773	1.00	27.53	1DIK1863
ATOM	1772	C	THR	235	-19.506	35.104	37.728	1.00	28.27	1DIK1864
ATOM	1773	O	THR	235	-19.098	35.065	36.565	1.00	27.05	1DIK1865
ATOM	1774	CB	THR	235	-17.513	35.272	39.329	1.00	26.76	1DIK1866
ATOM	1775	OG1	THR	235	-17.866	33.998	39.876	1.00	28.53	1DIK1867
ATOM	1776	CG2	THR	235	-16.859	36.104	40.416	1.00	27.73	1DIK1868
ATOM	1777	N	TYR	236	-20.575	34.406	38.129	1.00	27.79	1DIK1869
ATOM	1778	CA	TYR	236	-21.339	33.577	37.188	1.00	27.49	1DIK1870
ATOM	1779	C	TYR	236	-22.024	34.490				

Figure 8/23

ATOM	1793	CB	LEU	237	-23.813	37.734	36.682	1.00	25.77	IDIK1885
ATOM	1794	CG	LEU	237	-25.081	37.327	37.447	1.00	22.88	IDIK1886
ATOM	1795	CD1	LEU	237	-25.528	38.415	38.421	1.00	24.36	IDIK1887
ATOM	1796	CD2	LEU	237	-26.165	37.036	36.455	1.00	17.71	IDIK1888
ATOM	1797	N	MET	238	-20.940	37.423	35.286	1.00	24.39	IDIK1889
ATOM	1798	CA	MET	238	-19.918	37.948	34.403	1.00	25.37	IDIK1890
ATOM	1799	C	MET	238	-19.575	36.882	33.359	1.00	28.12	IDIK1891
ATOM	1800	O	MET	238	-19.335	37.210	32.195	1.00	31.98	IDIK1892
ATOM	1801	CB	MET	238	-18.684	38.358	35.203	1.00	21.01	IDIK1893
ATOM	1802	CG	MET	238	-18.967	39.504	36.148	1.00	18.56	IDIK1894
ATOM	1803	SD	MET	238	-17.500	40.183	36.915	1.00	26.85	IDIK1895
ATOM	1804	CE	MET	238	-16.964	41.396	35.681	1.00	20.81	IDIK1896
ATOM	1805	N	ASP	239	-19.562	35.608	33.764	1.00	29.27	IDIK1897
ATOM	1806	CA	ASP	239	-19.268	34.497	32.838	1.00	28.12	IDIK1898
ATOM	1807	C	ASP	239	-20.314	34.486	31.727	1.00	26.51	IDIK1899
ATOM	1808	O	ASP	239	-20.003	34.210	30.577	1.00	27.19	IDIK1900
ATOM	1809	CB	ASP	239	-19.340	33.129	33.542	1.00	27.22	IDIK1901
ATOM	1810	CG	ASP	239	-18.144	32.836	34.448	1.00	24.04	IDIK1902
ATOM	1811	OD1	ASP	239	-17.162	33.602	34.461	1.00	22.09	IDIK1903
ATOM	1812	OD2	ASP	239	-18.194	31.807	35.162	1.00	27.85	IDIK1904
ATOM	1813	N	MET	240	-21.557	34.784	32.089	1.00	24.64	IDIK1905
ATOM	1814	CA	MET	240	-22.664	34.800	31.141	1.00	26.17	IDIK1906
ATOM	1815	C	MET	240	-22.509	35.815	30.018	1.00	26.18	IDIK1907
ATOM	1816	O	MET	240	-23.034	35.621	28.924	1.00	25.09	IDIK1908
ATOM	1817	CB	MET	240	-23.984	35.039	31.877	1.00	29.12	IDIK1909
ATOM	1818	CG	MET	240	-24.519	33.809	32.591	1.00	28.59	IDIK1910
ATOM	1819	SD	MET	240	-24.873	32.469	31.404	1.00	34.30	IDIK1911
ATOM	1820	CE	MET	240	-26.354	33.141	30.505	1.00	25.69	IDIK1912
ATOM	1821	N	CYS	241	-21.793	36.899	30.280	1.00	25.30	IDIK1913
ATOM	1822	CA	CYS	241	-21.581	37.910	29.254	1.00	27.89	IDIK1914
ATOM	1823	C	CYS	241	-20.931	37.244	28.032	1.00	25.49	IDIK1915
ATOM	1824	O	CYS	241	-21.348	37.459	26.892	1.00	26.76	IDIK1916
ATOM	1825	CB	CYS	241	-20.710	39.049	29.814	1.00	24.99	IDIK1917
ATOM	1826	SG	CYS	241	-19.856	40.115	28.598	1.00	27.44	IDIK1918
ATOM	1827	N	SER	242	-19.924	36.420	28.291	1.00	25.28	IDIK1919
ATOM	1828	CA	SER	242	-19.197	35.698	27.256	1.00	25.73	IDIK1920
ATOM	1829	C	SER	242	-20.072	34.679	26.507	1.00	26.63	IDIK1921
ATOM	1830	O	SER	242	-20.275	34.786	25.289	1.00	25.57	IDIK1922
ATOM	1831	CB	SER	242	-18.003	34.989	27.897	1.00	27.44	IDIK1923
ATOM	1832	OG	SER	242	-17.294	34.219	26.949	1.00	39.33	IDIK1924
ATOM	1833	N	PHE	243	-20.594	33.697	27.238	1.00	26.85	IDIK1925
ATOM	1834	CA	PHE	243	-21.419	32.642	26.648	1.00	26.10	IDIK1926
ATOM	1835	C	PHE	243	-22.663	33.140	25.941	1.00	27.04	IDIK1927
ATOM	1836	O	PHE	243	-23.021	32.637	24.872	1.00	26.53	IDIK1928
ATOM	1837	CB	PHE	243	-21.818	31.617	27.714	1.00	25.98	IDIK1929
ATOM	1838	CG	PHE	243	-20.655	30.845	28.277	1.00	26.19	IDIK1930
ATOM	1839	CD1	PHE	243	-20.075	29.805	27.549	1.00	23.12	IDIK1931
ATOM	1840	CD2	PHE	243	-20.129	31.168	29.530	1.00	21.56	IDIK1932
ATOM	1841	CE1	PHE	243	-18.978	29.093	28.066	1.00	25.40	IDIK1933
ATOM	1842	CE2	PHE	243	-19.042	30.469	30.052	1.00	22.05	IDIK1934
ATOM	1843	CZ	PHE	243	-18.461	29.427	29.319	1.00	21.32	IDIK1935
ATOM	1844	N	ASP	244	-23.330	34.126	26.529	1.00	27.71	IDIK1936
ATOM	1845	CA	ASP	244	-24.537	34.643	25.907	1.00	30.62	IDIK1937
ATOM	1846	C	ASP	244	-24.235	35.494	24.666	1.00	32.18	IDIK1938
ATOM	1847	O	ASP	244	-25.120	35.741	23.854	1.00	34.05	IDIK1939
ATOM	1848	CB	ASP	244	-25.379	35.428	26.917	1.00	27.50	IDIK1940
ATOM	1849	CG	ASP	244	-26.785	35.723	26.404	1.00	28.82	IDIK1941
ATOM	1850	OD1	ASP	244	-27.531	34.777	26.077	1.00	24.13	IDIK1942
ATOM	1851	OD2	ASP	244	-27.149	36.910	26.323	1.00	30.15	IDIK1943
ATOM	1852	N	THR	245	-22.996	35.944	24.510	1.00	32.39	IDIK1944
ATOM	1853	CA	THR	245	-22.658	36.740	23.343	1.00	33.50	IDIK1945
ATOM	1854	C	THR	245	-22.282	35.850	22.153	1.00	38.87	IDIK1946
ATOM	1855	O	THR	245	-22.911	35.918	21.091	1.00	37.64	IDIK1947
ATOM	1856	CB	THR	245	-21.511	37.706	23.647	1.00	32.72	IDIK1948
ATOM	1857	OG1	THR	245	-21.940	38.652	24.631	1.00	37.51	IDIK1949
ATOM	1858	CG2	THR	245	-21.084	38.446	22.394	1.00	28.33	IDIK1950
ATOM	1859	N	ILE	246	-21.268	35.008	22.335	1.00	40.95	IDIK1951
ATOM	1860	CA	ILE	246	-20.803	34.140	21.262	1.00	43.89	IDIK1952
ATOM	1861	C	ILE	246	-21.590	32.847	21.034	1.00	48.67	IDIK1953
ATOM	1862	O	ILE	246	-21.151	31.992	20.262	1.00	48.67	IDIK1954
ATOM	1863	CB	ILE	246	-19.279	33.826	21.419	1.00	41.80	IDIK1955
ATOM	1864	CG1	ILE	246	-18.988	33.144	22.757	1.00	37.29	IDIK1956
ATOM	1865	CG2	ILE	246	-18.464	35.125	21.329	1.00	43.70	IDIK1957
ATOM	1866	CD								

Figure 8/24

ATOM	1878	OG1	THR	248	-26.917	33.299	18.699	1.00	74.12	IDIK1970
ATOM	1879	CG2	THR	248	-26.262	33.888	16.427	1.00	72.58	IDIK1971
ATOM	1880	N	THR	253	-23.919	38.646	16.591	1.00	49.08	IDIK1972
ATOM	1881	CA	THR	253	-24.110	39.972	15.999	1.00	51.56	IDIK1973
ATOM	1882	C	THR	253	-24.258	41.028	17.100	1.00	49.54	IDIK1974
ATOM	1883	O	THR	253	-23.757	42.146	16.965	1.00	49.39	IDIK1975
ATOM	1884	CB	THR	253	-25.394	40.051	15.103	1.00	52.26	IDIK1976
ATOM	1885	OG1	THR	253	-25.489	38.881	14.282	1.00	61.78	IDIK1977
ATOM	1886	CG2	THR	253	-25.344	41.284	14.189	1.00	51.28	IDIK1978
ATOM	1887	N	LYS	254	-24.941	40.670	18.185	1.00	46.23	IDIK1979
ATOM	1888	CA	LYS	254	-25.170	41.610	19.275	1.00	45.73	IDIK1980
ATOM	1889	C	LYS	254	-24.562	41.222	20.618	1.00	42.99	IDIK1981
ATOM	1890	O	LYS	254	-24.470	40.044	20.939	1.00	45.43	IDIK1982
ATOM	1891	CB	LYS	254	-26.664	41.864	19.410	1.00	46.12	IDIK1983
ATOM	1892	CG	LYS	254	-27.214	42.520	18.157	1.00	51.91	IDIK1984
ATOM	1893	CD	LYS	254	-28.671	42.840	18.273	1.00	56.51	IDIK1985
ATOM	1894	CE	LYS	254	-29.168	43.456	16.987	1.00	60.44	IDIK1986
ATOM	1895	NZ	LYS	254	-30.576	43.918	17.160	1.00	67.71	IDIK1987
ATOM	1896	N	LEU	255	-24.141	42.226	21.387	1.00	38.90	IDIK1988
ATOM	1897	CA	LEU	255	-23.533	42.022	22.705	1.00	33.29	IDIK1989
ATOM	1898	C	LEU	255	-24.584	41.661	23.751	1.00	32.90	IDIK1990
ATOM	1899	O	LEU	255	-25.637	42.288	23.825	1.00	33.07	IDIK1991
ATOM	1900	CB	LEU	255	-22.797	43.286	23.141	1.00	25.06	IDIK1992
ATOM	1901	CG	LEU	255	-21.856	43.213	24.344	1.00	26.05	IDIK1993
ATOM	1902	CD1	LEU	255	-20.707	42.242	24.095	1.00	21.04	IDIK1994
ATOM	1903	CD2	LEU	255	-21.326	44.595	24.608	1.00	22.14	IDIK1995
ATOM	1904	N	SER	256	-24.293	40.647	24.558	1.00	32.93	IDIK1996
ATOM	1905	CA	SER	256	-25.212	40.207	25.598	1.00	31.52	IDIK1997
ATOM	1906	C	SER	256	-25.489	41.293	26.643	1.00	32.01	IDIK1998
ATOM	1907	O	SER	256	-24.574	42.013	27.082	1.00	30.64	IDIK1999
ATOM	1908	CB	SER	256	-24.650	38.965	26.306	1.00	30.76	IDIK2000
ATOM	1909	OG	SER	256	-25.446	38.602	27.430	1.00	27.78	IDIK2001
ATOM	1910	N	PRO	257	-26.766	41.432	27.051	1.00	32.46	IDIK2002
ATOM	1911	CA	PRO	257	-27.131	42.434	28.060	1.00	32.73	IDIK2003
ATOM	1912	C	PRO	257	-26.372	42.191	29.379	1.00	31.79	IDIK2004
ATOM	1913	O	PRO	257	-26.136	43.130	30.138	1.00	35.33	IDIK2005
ATOM	1914	CB	PRO	257	-28.644	42.239	28.209	1.00	32.20	IDIK2006
ATOM	1915	CG	PRO	257	-29.053	41.696	26.861	1.00	31.42	IDIK2007
ATOM	1916	CD	PRO	257	-27.960	40.701	26.587	1.00	30.36	IDIK2008
ATOM	1917	N	PHE	258	-25.984	40.941	29.646	1.00	27.64	IDIK2009
ATOM	1918	CA	PHE	258	-25.221	40.617	30.859	1.00	25.04	IDIK2010
ATOM	1919	C	PHE	258	-23.910	41.407	30.928	1.00	24.80	IDIK2011
ATOM	1920	O	PHE	258	-23.389	41.661	32.011	1.00	22.95	IDIK2012
ATOM	1921	CB	PHE	258	-24.877	39.122	30.911	1.00	25.72	IDIK2013
ATOM	1922	CG	PHE	258	-26.033	38.239	31.253	1.00	24.20	IDIK2014
ATOM	1923	CD1	PHE	258	-26.455	38.105	32.569	1.00	23.98	IDIK2015
ATOM	1924	CD2	PHE	258	-26.712	37.544	30.257	1.00	26.82	IDIK2016
ATOM	1925	CE1	PHE	258	-27.543	37.288	32.890	1.00	23.72	IDIK2017
ATOM	1926	CE2	PHE	258	-27.806	36.721	30.565	1.00	24.56	IDIK2018
ATOM	1927	CZ	PHE	258	-28.220	36.594	31.879	1.00	24.85	IDIK2019
ATOM	1928	N	CYS	259	-23.375	41.790	29.772	1.00	24.43	IDIK2020
ATOM	1929	CA	CYS	259	-22.119	42.536	29.731	1.00	27.30	IDIK2021
ATOM	1930	C	CYS	259	-22.323	43.952	30.207	1.00	29.38	IDIK2022
ATOM	1931	O	CYS	259	-21.420	44.565	30.771	1.00	29.68	IDIK2023
ATOM	1932	CB	CYS	259	-21.564	42.591	28.307	1.00	26.45	IDIK2024
ATOM	1933	SG	CYS	259	-21.348	40.968	27.516	1.00	30.19	IDIK2025
ATOM	1934	N	ASP	260	-23.527	44.460	29.975	1.00	31.11	IDIK2026
ATOM	1935	CA	ASP	260	-23.879	45.821	30.326	1.00	33.64	IDIK2027
ATOM	1936	C	ASP	260	-24.002	46.070	31.815	1.00	32.59	IDIK2028
ATOM	1937	O	ASP	260	-24.054	47.212	32.246	1.00	34.03	IDIK2029
ATOM	1938	CB	ASP	260	-25.194	46.201	29.645	1.00	39.78	IDIK2030
ATOM	1939	CG	ASP	260	-25.246	47.667	29.252	1.00	44.26	IDIK2031
ATOM	1940	OD1	ASP	260	-24.190	48.185	28.834	1.00	45.01	IDIK2032
ATOM	1941	OD2	ASP	260	-26.328	48.292	29.362	1.00	42.47	IDIK2033
ATOM	1942	N	LEU	261	-24.051	45.007	32.603	1.00	33.47	IDIK2034
ATOM	1943	CA	LEU	261	-24.200	45.149	34.043	1.00	29.07	IDIK2035
ATOM	1944	C	LEU	261	-22.887	45.446	34.736	1.00	29.71	IDIK2036
ATOM	1945	O	LEU	261	-22.867	45.747	35.929	1.00	33.17	IDIK2037
ATOM	1946	CB	LEU	261	-24.816	43.880	34.629	1.00	28.55	IDIK2038
ATOM	1947	CG	LEU	261	-26.103	43.405	33.947	1.00	27.56	IDIK2039
ATOM	1948	CD1	LEU	261	-26.541	42.089	34.534	1.00	25.79	IDIK2040
ATOM	1949	CD2	LEU	261	-27.197	44.441	34.130	1.00	27.02	IDIK2041
ATOM	1950	N								

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ATOM	1963	C	THR	263	-16.811	47.961	33.425	1.00	29.54	1DIK2055
ATOM	1964	O	THR	263	-16.466	46.805	33.671	1.00	31.34	1DIK2056
ATOM	1965	CB	THR	263	-17.860	49.648	34.985	1.00	32.12	1DIK2057
ATOM	1966	OG1	THR	263	-16.998	49.193	36.036	1.00	29.58	1DIK2058
ATOM	1967	CG2	THR	263	-19.183	50.112	35.589	1.00	22.67	1DIK2059
ATOM	1968	N	HIS	264	-16.087	48.802	32.693	1.00	30.02	1DIK2060
ATOM	1969	CA	HIS	264	-14.829	48.400	32.090	1.00	28.00	1DIK2061
ATOM	1970	C	HIS	264	-13.717	47.984	33.052	1.00	30.02	1DIK2062
ATOM	1971	O	HIS	264	-12.998	47.015	32.774	1.00	31.35	1DIK2063
ATOM	1972	CB	HIS	264	-14.314	49.480	31.143	1.00	27.91	1DIK2064
ATOM	1973	CG	HIS	264	-13.111	49.048	30.370	1.00	34.68	1DIK2065
ATOM	1974	ND1	HIS	264	-13.186	48.157	29.318	1.00	31.27	1DIK2066
ATOM	1975	CD2	HIS	264	-11.795	49.339	30.527	1.00	35.74	1DIK2067
ATOM	1976	CE1	HIS	264	-11.969	47.916	28.863	1.00	37.49	1DIK2068
ATOM	1977	NE2	HIS	264	-11.108	48.620	29.579	1.00	38.67	1DIK2069
ATOM	1978	N	ASP	265	-13.560	48.703	34.167	1.00	31.42	1DIK2070
ATOM	1979	CA	ASP	265	-12.533	48.371	35.172	1.00	29.27	1DIK2071
ATOM	1980	C	ASP	265	-12.831	47.030	35.859	1.00	27.71	1DIK2072
ATOM	1981	O	ASP	265	-11.923	46.352	36.346	1.00	25.15	1DIK2073
ATOM	1982	CB	ASP	265	-12.421	49.481	36.222	1.00	36.26	1DIK2074
ATOM	1983	CG	ASP	265	-13.745	49.764	36.921	1.00	44.48	1DIK2075
ATOM	1984	OD1	ASP	265	-14.671	50.307	36.267	1.00	43.98	1DIK2076
ATOM	1985	OD2	ASP	265	-13.860	49.441	38.128	1.00	49.77	1DIK2077
ATOM	1986	N	GLU	266	-14.108	46.651	35.896	1.00	26.27	1DIK2078
ATOM	1987	CA	GLU	266	-14.502	45.378	36.484	1.00	26.01	1DIK2079
ATOM	1988	C	GLU	266	-14.093	44.272	35.517	1.00	27.04	1DIK2080
ATOM	1989	O	GLU	266	-13.665	43.205	35.956	1.00	28.64	1DIK2081
ATOM	1990	CB	GLU	266	-15.997	45.359	36.785	1.00	24.19	1DIK2082
ATOM	1991	CG	GLU	266	-16.336	46.287	37.939	1.00	24.01	1DIK2083
ATOM	1992	CD	GLU	266	-17.824	46.521	38.139	1.00	28.94	1DIK2084
ATOM	1993	OE1	GLU	266	-18.647	46.091	37.299	1.00	30.18	1DIK2085
ATOM	1994	OE2	GLU	266	-18.175	47.150	39.160	1.00	32.29	1DIK2086
ATOM	1995	N	TRP	267	-14.207	44.521	34.210	1.00	24.96	1DIK2087
ATOM	1996	CA	TRP	267	-13.765	43.535	33.221	1.00	24.91	1DIK2088
ATOM	1997	C	TRP	267	-12.243	43.380	33.306	1.00	24.45	1DIK2089
ATOM	1998	O	TRP	267	-11.723	42.269	33.202	1.00	25.00	1DIK2090
ATOM	1999	CB	TRP	267	-14.210	43.915	31.801	1.00	22.45	1DIK2091
ATOM	2000	CG	TRP	267	-15.684	43.646	31.596	1.00	22.28	1DIK2092
ATOM	2001	CD1	TRP	267	-16.661	44.567	31.355	1.00	20.97	1DIK2093
ATOM	2002	CD2	TRP	267	-16.349	42.370	31.684	1.00	20.83	1DIK2094
ATOM	2003	NE1	TRP	267	-17.889	43.952	31.293	1.00	23.15	1DIK2095
ATOM	2004	CE2	TRP	267	-17.726	42.604	31.493	1.00	23.26	1DIK2096
ATOM	2005	CE3	TRP	267	-15.913	41.055	31.914	1.00	18.67	1DIK2097
ATOM	2006	CZ2	TRP	267	-18.672	41.569	31.529	1.00	22.56	1DIK2098
ATOM	2007	CZ3	TRP	267	-16.849	40.032	31.951	1.00	15.00	1DIK2099
ATOM	2008	CH2	TRP	267	-18.211	40.294	31.761	1.00	18.10	1DIK2100
ATOM	2009	N	ILE	268	-11.526	44.479	33.517	1.00	23.42	1DIK2101
ATOM	2010	CA	ILE	268	-10.073	44.399	33.647	1.00	25.35	1DIK2102
ATOM	2011	C	ILE	268	-9.721	43.461	34.801	1.00	27.88	1DIK2103
ATOM	2012	O	ILE	268	-8.776	42.673	34.714	1.00	28.12	1DIK2104
ATOM	2013	CB	ILE	268	-9.460	45.786	33.889	1.00	27.94	1DIK2105
ATOM	2014	CG1	ILE	268	-9.515	46.575	32.579	1.00	27.22	1DIK2106
ATOM	2015	CG2	ILE	268	-8.031	45.659	34.457	1.00	19.33	1DIK2107
ATOM	2016	CD1	ILE	268	-9.124	48.027	32.704	1.00	36.44	1DIK2108
ATOM	2017	N	ASN	269	-10.495	43.553	35.877	1.00	27.63	1DIK2109
ATOM	2018	CA	ASN	269	-10.290	42.704	37.039	1.00	27.33	1DIK2110
ATOM	2019	C	ASN	269	-10.656	41.259	36.739	1.00	26.62	1DIK2111
ATOM	2020	O	ASN	269	-9.918	40.348	37.108	1.00	27.01	1DIK2112
ATOM	2021	CB	ASN	269	-11.110	43.206	38.226	1.00	32.36	1DIK2113
ATOM	2022	CG	ASN	269	-10.427	44.332	38.966	1.00	32.62	1DIK2114
ATOM	2023	OD1	ASN	269	-9.287	44.208	39.423	1.00	29.54	1DIK2115
ATOM	2024	ND2	ASN	269	-11.120	45.443	39.088	1.00	38.68	1DIK2116
ATOM	2025	N	TYR	270	-11.794	41.052	36.075	1.00	22.76	1DIK2117
ATOM	2026	CA	TYR	270	-12.245	39.708	35.712	1.00	22.97	1DIK2118
ATOM	2027	C	TYR	270	-11.168	39.013	34.866	1.00	25.78	1DIK2119
ATOM	2028	O	TYR	270	-10.788	37.868	35.135	1.00	27.56	1DIK2120
ATOM	2029	CB	TYR	270	-13.559	39.800	34.934	1.00	22.99	1DIK2121
ATOM	2030	CG	TYR	270	-14.101	38.485	34.386	1.00	25.74	1DIK2122
ATOM	2031	CD1	TYR	270	-14.989	37.699	35.134	1.00	26.53	1DIK2123
ATOM	2032	CD2	TYR	270	-13.761	38.050	33.099	1.00	23.95	1DIK2124
ATOM	2033	CE1	TYR	270	-15.528	36.511	34.607	1.00	23.23	1DIK2125
ATOM	2034	CE2	TYR	270	-14					

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ATOM	2048	O	TYR	272	-6.308	37.209	36.738	1.00	27.60	1DIK2140
ATOM	2049	CB	TYR	272	-6.546	40.458	36.501	1.00	25.93	1DIK2141
ATOM	2050	CG	TYR	272	-5.236	40.246	37.210	1.00	24.39	1DIK2142
ATOM	2051	CD1	TYR	272	-4.042	40.250	36.495	1.00	24.69	1DIK2143
ATOM	2052	CD2	TYR	272	-5.186	40.001	38.587	1.00	24.58	1DIK2144
ATOM	2053	CE1	TYR	272	-2.825	40.014	37.120	1.00	24.93	1DIK2145
ATOM	2054	CE2	TYR	272	-3.970	39.762	39.230	1.00	23.27	1DIK2146
ATOM	2055	CZ	TYR	272	-2.794	39.770	38.482	1.00	25.13	1DIK2147
ATOM	2056	OH	TYR	272	-1.577	39.541	39.073	1.00	27.21	1DIK2148
ATOM	2057	N	LEU	273	-8.441	37.900	36.969	1.00	24.96	1DIK2149
ATOM	2058	CA	LEU	273	-8.834	36.743	37.778	1.00	24.02	1DIK2150
ATOM	2059	C	LEU	273	-8.624	35.455	36.964	1.00	25.27	1DIK2151
ATOM	2060	O	LEU	273	-8.159	34.454	37.503	1.00	29.71	1DIK2152
ATOM	2061	CB	LEU	273	-10.302	36.858	38.214	1.00	20.23	1DIK2153
ATOM	2062	CG	LEU	273	-10.976	35.622	38.826	1.00	23.41	1DIK2154
ATOM	2063	CD1	LEU	273	-10.254	35.191	40.104	1.00	20.60	1DIK2155
ATOM	2064	CD2	LEU	273	-12.440	35.922	39.108	1.00	17.70	1DIK2156
ATOM	2065	N	GLN	274	-8.962	35.478	35.672	1.00	23.99	1DIK2157
ATOM	2066	CA	GLN	274	-8.778	34.303	34.811	1.00	21.73	1DIK2158
ATOM	2067	C	GLN	274	-7.290	33.944	34.655	1.00	21.38	1DIK2159
ATOM	2068	O	GLN	274	-6.928	32.763	34.650	1.00	19.72	1DIK2160
ATOM	2069	CB	GLN	274	-9.415	34.530	33.442	1.00	20.31	1DIK2161
ATOM	2070	CG	GLN	274	-10.881	34.906	33.505	1.00	23.01	1DIK2162
ATOM	2071	CD	GLN	274	-11.710	34.017	34.424	1.00	25.47	1DIK2163
ATOM	2072	OE1	GLN	274	-11.536	32.805	34.477	1.00	23.72	1DIK2164
ATOM	2073	NE2	GLN	274	-12.622	34.629	35.154	1.00	32.39	1DIK2165
ATOM	2074	N	SER	275	-6.436	34.961	34.526	1.00	20.92	1DIK2166
ATOM	2075	CA	SER	275	-4.991	34.751	34.433	1.00	20.81	1DIK2167
ATOM	2076	C	SER	275	-4.472	34.099	35.725	1.00	24.14	1DIK2168
ATOM	2077	O	SER	275	-3.612	33.208	35.684	1.00	27.93	1DIK2169
ATOM	2078	CB	SER	275	-4.271	36.078	34.205	1.00	15.74	1DIK2170
ATOM	2079	OG	SER	275	-4.640	36.626	32.950	1.00	24.68	1DIK2171
ATOM	2080	N	LEU	276	-4.991	34.537	36.873	1.00	25.40	1DIK2172
ATOM	2081	CA	LEU	276	-4.571	33.969	38.157	1.00	25.08	1DIK2173
ATOM	2082	C	LEU	276	-4.956	32.500	38.259	1.00	22.91	1DIK2174
ATOM	2083	O	LEU	276	-4.132	31.675	38.619	1.00	24.12	1DIK2175
ATOM	2084	CB	LEU	276	-5.173	34.753	39.333	1.00	25.80	1DIK2176
ATOM	2085	CG	LEU	276	-4.558	36.123	39.596	1.00	23.07	1DIK2177
ATOM	2086	CD1	LEU	276	-5.418	36.893	40.560	1.00	23.03	1DIK2178
ATOM	2087	CD2	LEU	276	-3.158	35.948	40.144	1.00	24.41	1DIK2179
ATOM	2088	N	LYS	277	-6.204	32.174	37.943	1.00	24.32	1DIK2180
ATOM	2089	CA	LYS	277	-6.656	30.790	38.001	1.00	25.45	1DIK2181
ATOM	2090	C	LYS	277	-5.722	29.874	37.204	1.00	24.92	1DIK2182
ATOM	2091	O	LYS	277	-5.302	28.835	37.703	1.00	26.63	1DIK2183
ATOM	2092	CB	LYS	277	-8.049	30.647	37.417	1.00	26.65	1DIK2184
ATOM	2093	CG	LYS	277	-9.226	31.126	38.222	1.00	30.58	1DIK2185
ATOM	2094	CD	LYS	277	-10.424	30.639	37.399	1.00	36.27	1DIK2186
ATOM	2095	CE	LYS	277	-11.754	31.247	37.737	1.00	39.17	1DIK2187
ATOM	2096	NZ	LYS	277	-12.677	30.913	36.604	1.00	37.60	1DIK2188
ATOM	2097	N	LYS	278	-5.408	30.250	35.964	1.00	24.38	1DIK2189
ATOM	2098	CA	LYS	278	-4.523	29.440	35.111	1.00	24.41	1DIK2190
ATOM	2099	C	LYS	278	-3.073	29.414	35.598	1.00	24.27	1DIK2191
ATOM	2100	O	LYS	278	-2.429	28.360	35.590	1.00	24.08	1DIK2192
ATOM	2101	CB	LYS	278	-4.544	29.948	33.659	1.00	23.48	1DIK2193
ATOM	2102	CG	LYS	278	-5.880	29.828	32.975	1.00	20.48	1DIK2194
ATOM	2103	CD	LYS	278	-6.423	28.428	33.097	1.00	19.64	1DIK2195
ATOM	2104	CE	LYS	278	-7.859	28.389	32.661	1.00	24.74	1DIK2196
ATOM	2105	NZ	LYS	278	-8.431	27.043	32.798	1.00	22.55	1DIK2197
ATOM	2106	N	TYR	279	-2.565	30.573	36.016	1.00	22.37	1DIK2198
ATOM	2107	CA	TYR	279	-1.194	30.686	36.488	1.00	22.48	1DIK2199
ATOM	2108	C	TYR	279	-0.880	29.887	37.749	1.00	24.45	1DIK2200
ATOM	2109	O	TYR	279	0.165	29.237	37.826	1.00	25.51	1DIK2201
ATOM	2110	CB	TYR	279	-0.828	32.141	36.724	1.00	23.08	1DIK2202
ATOM	2111	CG	TYR	279	0.618	32.318	37.123	1.00	25.86	1DIK2203
ATOM	2112	CD1	TYR	279	1.631	32.222	36.179	1.00	21.81	1DIK2204
ATOM	2113	CD2	TYR	279	0.973	32.570	38.452	1.00	24.65	1DIK2205
ATOM	2114	CE1	TYR	279	2.956	32.368	36.540	1.00	26.71	1DIK2206
ATOM	2115	CE2	TYR	279	2.294	32.718	38.824	1.00	21.38	1DIK2207
ATOM	2116	CZ	TYR	279	3.281	32.616	37.863	1.00	25.91	1DIK2208
ATOM	2117	OH	TYR	279	4.596	32.746	38.217	1.00	28.30	1DIK2209
ATOM	2118	N	TYR	280	-1.764	29.938	38.740	1.00	24.59	1DIK2210
ATOM	2119	CA	TYR	280	-1.536	29.208	39.981			

Figure 8/27

ATOM	2133	O	GLY	281	-2.512	24.122	38.342	1.00	29.22	1DIK2225
ATOM	2134	N	HIS	282	-2.141	25.771	36.841	1.00	22.24	1DIK2226
ATOM	2135	CA	HIS	282	-1.342	24.943	35.939	1.00	24.32	1DIK2227
ATOM	2136	C	HIS	282	-0.042	25.561	35.448	1.00	26.33	1DIK2228
ATOM	2137	O	HIS	282	0.770	24.877	34.817	1.00	27.62	1DIK2229
ATOM	2138	CB	HIS	282	-2.190	24.543	34.733	1.00	21.27	1DIK2230
ATOM	2139	CG	HIS	282	-3.524	23.985	35.112	1.00	29.02	1DIK2231
ATOM	2140	ND1	HIS	282	-3.765	22.631	35.222	1.00	29.69	1DIK2232
ATOM	2141	CD2	HIS	282	-4.685	24.602	35.444	1.00	29.92	1DIK2233
ATOM	2142	CE1	HIS	282	-5.015	22.437	35.605	1.00	30.68	1DIK2234
ATOM	2143	NE2	HIS	282	-5.595	23.617	35.747	1.00	30.72	1DIK2235
ATOM	2144	N	GLY	283	0.155	26.846	35.722	1.00	27.84	1DIK2236
ATOM	2145	CA	GLY	283	1.370	27.508	35.292	1.00	26.80	1DIK2237
ATOM	2146	C	GLY	283	2.436	27.399	36.365	1.00	30.11	1DIK2238
ATOM	2147	O	GLY	283	2.324	26.566	37.272	1.00	26.73	1DIK2239
ATOM	2148	N	ALA	284	3.461	28.249	36.259	1.00	31.03	1DIK2240
ATOM	2149	CA	ALA	284	4.579	28.284	37.196	1.00	28.74	1DIK2241
ATOM	2150	C	ALA	284	4.178	28.654	38.621	1.00	32.24	1DIK2242
ATOM	2151	O	ALA	284	4.955	28.464	39.553	1.00	36.63	1DIK2243
ATOM	2152	CB	ALA	284	5.626	29.240	36.702	1.00	26.23	1DIK2244
ATOM	2153	N	GLY	285	2.974	29.182	38.800	1.00	31.80	1DIK2245
ATOM	2154	CA	GLY	285	2.534	29.541	40.133	1.00	30.04	1DIK2246
ATOM	2155	C	GLY	285	2.289	28.305	40.969	1.00	32.15	1DIK2247
ATOM	2156	O	GLY	285	2.274	28.364	42.201	1.00	39.54	1DIK2248
ATOM	2157	N	ASN	286	2.090	27.174	40.307	1.00	29.49	1DIK2249
ATOM	2158	CA	ASN	286	1.844	25.921	41.001	1.00	26.41	1DIK2250
ATOM	2159	C	ASN	286	3.140	25.106	41.045	1.00	28.02	1DIK2251
ATOM	2160	O	ASN	286	3.825	24.958	40.031	1.00	29.27	1DIK2252
ATOM	2161	CB	ASN	286	0.747	25.148	40.278	1.00	22.60	1DIK2253
ATOM	2162	CG	ASN	286	0.176	24.038	41.118	1.00	25.66	1DIK2254
ATOM	2163	OD1	ASN	286	0.822	23.009	41.330	1.00	27.94	1DIK2255
ATOM	2164	ND2	ASN	286	-1.039	24.236	41.611	1.00	22.58	1DIK2256
ATOM	2165	N	PRO	287	3.506	24.576	42.225	1.00	30.51	1DIK2257
ATOM	2166	CA	PRO	287	4.739	23.780	42.340	1.00	31.36	1DIK2258
ATOM	2167	C	PRO	287	4.852	22.670	41.288	1.00	31.71	1DIK2259
ATOM	2168	O	PRO	287	5.931	22.427	40.750	1.00	34.15	1DIK2260
ATOM	2169	CB	PRO	287	4.658	23.221	43.762	1.00	29.15	1DIK2261
ATOM	2170	CG	PRO	287	3.923	24.320	44.499	1.00	32.66	1DIK2262
ATOM	2171	CD	PRO	287	2.821	24.691	43.527	1.00	29.14	1DIK2263
ATOM	2172	N	LEU	288	3.741	22.000	40.992	1.00	31.66	1DIK2264
ATOM	2173	CA	LEU	288	3.734	20.926	39.999	1.00	30.96	1DIK2265
ATOM	2174	C	LEU	288	3.054	21.320	38.673	1.00	31.70	1DIK2266
ATOM	2175	O	LEU	288	2.710	20.447	37.861	1.00	32.44	1DIK2267
ATOM	2176	CB	LEU	288	3.071	19.673	40.584	1.00	27.59	1DIK2268
ATOM	2177	CG	LEU	288	3.854	19.025	41.731	1.00	27.62	1DIK2269
ATOM	2178	CD1	LEU	288	3.039	17.913	42.364	1.00	28.75	1DIK2270
ATOM	2179	CD2	LEU	288	5.177	18.502	41.206	1.00	25.46	1DIK2271
ATOM	2180	N	GLY	289	2.877	22.626	38.458	1.00	29.27	1DIK2272
ATOM	2181	CA	GLY	289	2.240	23.121	37.245	1.00	28.87	1DIK2273
ATOM	2182	C	GLY	289	3.038	22.806	35.990	1.00	28.45	1DIK2274
ATOM	2183	O	GLY	289	2.591	22.015	35.152	1.00	25.00	1DIK2275
ATOM	2184	N	PRO	290	4.227	23.414	35.827	1.00	26.67	1DIK2276
ATOM	2185	CA	PRO	290	5.075	23.169	34.654	1.00	27.05	1DIK2277
ATOM	2186	C	PRO	290	5.420	21.667	34.473	1.00	27.87	1DIK2278
ATOM	2187	O	PRO	290	5.590	21.194	33.349	1.00	28.39	1DIK2279
ATOM	2188	CB	PRO	290	6.312	24.034	34.945	1.00	25.95	1DIK2280
ATOM	2189	CG	PRO	290	5.756	25.161	35.778	1.00	22.17	1DIK2281
ATOM	2190	CD	PRO	290	4.851	24.402	36.728	1.00	24.69	1DIK2282
ATOM	2191	N	THR	291	5.521	20.925	35.576	1.00	28.55	1DIK2283
ATOM	2192	CA	THR	291	5.807	19.495	35.525	1.00	23.19	1DIK2284
ATOM	2193	C	THR	291	4.778	18.742	34.668	1.00	23.08	1DIK2285
ATOM	2194	O	THR	291	5.106	17.718	34.067	1.00	23.15	1DIK2286
ATOM	2195	CB	THR	291	5.862	18.902	36.958	1.00	21.42	1DIK2287
ATOM	2196	OG1	THR	291	7.129	19.213	37.530	1.00	19.92	1DIK2288
ATOM	2197	CG2	THR	291	5.684	17.395	36.968	1.00	14.25	1DIK2289
ATOM	2198	N	GLN	292	3.543	19.243	34.599	1.00	22.57	1DIK2290
ATOM	2199	CA	GLN	292	2.509	18.584	33.791	1.00	21.65	1DIK2291
ATOM	2200	C	GLN	292	2.805	18.650	32.283	1.00	19.91	1DIK2292
ATOM	2201	O	GLN	292	2.227	17.904	31.494	1.00	23.11	1DIK2293
ATOM	2202	CB	GLN	292	1.119	19.190	34.046	1.00	18.92	1DIK2294
ATOM	2203	CG	GLN	292	0.656	19.202	35.487	1.00	23.26	1DIK2295
ATOM	2204	CD	GLN	292	0.821	17.867	36.187	1.00	24.01	1DIK2296
ATOM	2205	OE1	GLN	29						

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ATOM	2218	N	GLY	295	6.205	15.815	29.609	1.00	17.01	1DIK2310
ATOM	2219	CA	GLY	295	6.003	14.701	28.692	1.00	16.78	1DIK2311
ATOM	2220	C	GLY	295	5.870	15.193	27.258	1.00	21.51	1DIK2312
ATOM	2221	O	GLY	295	6.561	14.697	26.345	1.00	20.80	1DIK2313
ATOM	2222	N	TYR	296	4.988	16.177	27.055	1.00	16.60	1DIK2314
ATOM	2223	CA	TYR	296	4.780	16.767	25.739	1.00	16.58	1DIK2315
ATOM	2224	C	TYR	296	6.063	17.410	25.193	1.00	20.08	1DIK2316
ATOM	2225	O	TYR	296	6.371	17.314	23.996	1.00	20.96	1DIK2317
ATOM	2226	CB	TYR	296	3.686	17.823	25.803	1.00	17.05	1DIK2318
ATOM	2227	CG	TYR	296	3.273	18.295	24.437	1.00	16.86	1DIK2319
ATOM	2228	CD1	TYR	296	2.388	17.541	23.676	1.00	17.02	1DIK2320
ATOM	2229	CD2	TYR	296	3.774	19.483	23.896	1.00	15.90	1DIK2321
ATOM	2230	CE1	TYR	296	2.006	17.942	22.418	1.00	16.51	1DIK2322
ATOM	2231	CE2	TYR	296	3.399	19.897	22.637	1.00	17.02	1DIK2323
ATOM	2232	CZ	TYR	296	2.510	19.117	21.899	1.00	20.60	1DIK2324
ATOM	2233	OH	TYR	296	2.101	19.495	20.640	1.00	22.06	1DIK2325
ATOM	2234	N	ALA	297	6.798	18.076	26.081	1.00	20.78	1DIK2326
ATOM	2235	CA	ALA	297	8.054	18.726	25.730	1.00	20.65	1DIK2327
ATOM	2236	C	ALA	297	9.079	17.698	25.239	1.00	18.75	1DIK2328
ATOM	2237	O	ALA	297	9.795	17.942	24.267	1.00	20.26	1DIK2329
ATOM	2238	CB	ALA	297	8.599	19.487	26.934	1.00	20.11	1DIK2330
ATOM	2239	N	ASN	298	9.156	16.549	25.904	1.00	14.67	1DIK2331
ATOM	2240	CA	ASN	298	10.088	15.507	25.479	1.00	15.91	1DIK2332
ATOM	2241	C	ASN	298	9.656	14.898	24.146	1.00	17.04	1DIK2333
ATOM	2242	O	ASN	298	10.498	14.429	23.373	1.00	18.62	1DIK2334
ATOM	2243	CB	ASN	298	10.226	14.433	26.553	1.00	16.51	1DIK2335
ATOM	2244	CG	ASN	298	11.093	14.088	27.702	1.00	19.39	1DIK2336
ATOM	2245	OD1	ASN	298	12.127	15.533	27.494	1.00	18.34	1DIK2337
ATOM	2246	ND2	ASN	298	10.686	14.559	28.919	1.00	10.95	1DIK2338
ATOM	2247	N	GLU	299	8.348	14.900	23.879	1.00	18.29	1DIK2339
ATOM	2248	CA	GLU	299	7.828	14.403	22.608	1.00	20.08	1DIK2340
ATOM	2249	C	GLU	299	8.214	15.404	21.515	1.00	19.66	1DIK2341
ATOM	2250	O	GLU	299	8.519	15.012	20.385	1.00	18.23	1DIK2342
ATOM	2251	CB	GLU	299	6.309	14.226	22.649	1.00	17.35	1DIK2343
ATOM	2252	CG	GLU	299	5.877	13.046	23.478	1.00	20.50	1DIK2344
ATOM	2253	CD	GLU	299	4.383	12.754	23.393	1.00	24.46	1DIK2345
ATOM	2254	OE1	GLU	299	3.576	13.690	23.181	1.00	17.82	1DIK2346
ATOM	2255	OE2	GLU	299	4.013	11.572	23.542	1.00	22.37	1DIK2347
ATOM	2256	N	LEU	300	8.206	16.693	21.859	1.00	19.59	1DIK2348
ATOM	2257	CA	LEU	300	8.596	17.739	20.917	1.00	20.13	1DIK2349
ATOM	2258	C	LEU	300	10.095	17.600	20.593	1.00	20.28	1DIK2350
ATOM	2259	O	LEU	300	10.487	17.665	19.422	1.00	22.61	1DIK2351
ATOM	2260	CB	LEU	300	8.289	19.125	21.488	1.00	21.25	1DIK2352
ATOM	2261	CG	LEU	300	8.649	20.287	20.559	1.00	24.96	1DIK2353
ATOM	2262	CD1	LEU	300	7.930	20.151	19.230	1.00	24.02	1DIK2354
ATOM	2263	CD2	LEU	300	8.269	21.578	21.219	1.00	16.85	1DIK2355
ATOM	2264	N	ILE	301	10.926	17.400	21.624	1.00	18.80	1DIK2356
ATOM	2265	CA	ILE	301	12.373	17.213	21.444	1.00	15.04	1DIK2357
ATOM	2266	C	ILE	301	12.587	16.017	20.484	1.00	20.56	1DIK2358
ATOM	2267	O	ILE	301	13.429	16.056	19.575	1.00	18.58	1DIK2359
ATOM	2268	CB	ILE	301	13.059	16.937	22.812	1.00	16.02	1DIK2360
ATOM	2269	CG1	ILE	301	13.004	18.194	23.686	1.00	17.32	1DIK2361
ATOM	2270	CG2	ILE	301	14.498	16.487	22.626	1.00	6.56	1DIK2362
ATOM	2271	CD1	ILE	301	13.594	18.005	25.064	1.00	14.26	1DIK2363
ATOM	2272	N	ALA	302	11.806	14.958	20.685	1.00	20.02	1DIK2364
ATOM	2273	CA	ALA	302	11.891	13.776	19.840	1.00	20.23	1DIK2365
ATOM	2274	C	ALA	302	11.610	14.139	18.375	1.00	21.81	1DIK2366
ATOM	2275	O	ALA	302	12.326	13.708	17.470	1.00	19.81	1DIK2367
ATOM	2276	CB	ALA	302	10.912	12.718	20.327	1.00	20.45	1DIK2368
ATOM	2277	N	ARG	303	10.577	14.943	18.138	1.00	20.13	1DIK2369
ATOM	2278	CA	ARG	303	10.227	15.329	16.774	1.00	17.34	1DIK2370
ATOM	2279	C	ARG	303	11.245	16.267	16.093	1.00	19.34	1DIK2371
ATOM	2280	O	ARG	303	11.569	16.095	14.907	1.00	15.37	1DIK2372
ATOM	2281	CB	ARG	303	8.816	15.934	16.750	1.00	15.85	1DIK2373
ATOM	2282	CG	ARG	303	7.715	14.914	17.021	1.00	12.30	1DIK2374
ATOM	2283	CD	ARG	303	6.351	15.572	17.215	1.00	11.98	1DIK2375
ATOM	2284	NE	ARG	303	5.287	14.572	17.315	1.00	11.60	1DIK2376
ATOM	2285	CZ	ARG	303	3.989	14.836	17.456	1.00	15.17	1DIK2377
ATOM	2286	NH1	ARG	303	3.538	16.088	17.540	1.00	11.46	1DIK2378
ATOM	2287	NH2	ARG	303	3.132	13.830	17.519	1.00	15.32	1DIK2379
ATOM	2288	N	LEU	304	11.752	17.247	16.838	1.00	16.06	1DIK2380
ATOM	2289	CA	LEU	304	12.722	18.188	16.289	1.00	18.27	1DIK2

Figure 8/29

ATOM	2303	N	HIS	306	14.276	14.100	15.476	1.00	24.74	1DIK2395
ATOM	2304	CA	HIS	306	13.982	12.815	14.815	1.00	28.44	1DIK2396
ATOM	2305	C	HIS	306	14.566	11.628	15.600	1.00	27.46	1DIK2397
ATOM	2306	O	HIS	306	15.122	10.704	15.012	1.00	33.56	1DIK2398
ATOM	2307	CB	HIS	306	14.519	12.796	13.374	1.00	27.83	1DIK2399
ATOM	2308	CG	HIS	306	14.236	14.053	12.613	1.00	33.95	1DIK2400
ATOM	2309	ND1	HIS	306	12.959	14.447	12.268	1.00	35.48	1DIK2401
ATOM	2310	CD2	HIS	306	15.065	15.022	12.155	1.00	32.87	1DIK2402
ATOM	2311	CE1	HIS	306	13.013	15.604	11.633	1.00	35.66	1DIK2403
ATOM	2312	NE2	HIS	306	14.280	15.974	11.552	1.00	35.02	1DIK2404
ATOM	2313	N	SER	307	14.429	11.654	16.919	1.00	22.90	1DIK2405
ATOM	2314	CA	SER	307	14.956	10.606	17.779	1.00	24.39	1DIK2406
ATOM	2315	C	SER	307	13.858	10.081	18.684	1.00	27.25	1DIK2407
ATOM	2316	O	SER	307	12.864	10.768	18.920	1.00	31.56	1DIK2408
ATOM	2317	CB	SER	307	16.050	11.175	18.662	1.00	22.96	1DIK2409
ATOM	2318	OG	SER	307	16.779	12.147	17.948	1.00	39.77	1DIK2410
ATOM	2319	N	PRO	308	14.014	8.845	19.201	1.00	28.75	1DIK2411
ATOM	2320	CA	PRO	308	13.004	8.260	20.094	1.00	26.08	1DIK2412
ATOM	2321	C	PRO	308	12.764	9.127	21.322	1.00	23.85	1DIK2413
ATOM	2322	O	PRO	308	13.614	9.921	21.711	1.00	22.93	1DIK2414
ATOM	2323	CB	PRO	308	13.609	6.899	20.450	1.00	25.36	1DIK2415
ATOM	2324	CG	PRO	308	14.416	6.567	19.204	1.00	24.66	1DIK2416
ATOM	2325	CD	PRO	308	15.109	7.886	18.963	1.00	25.37	1DIK2417
ATOM	2326	N	VAL	309	11.601	8.968	21.932	1.00	25.92	1DIK2418
ATOM	2327	CA	VAL	309	11.250	9.744	23.105	1.00	23.97	1DIK2419
ATOM	2328	C	VAL	309	11.959	9.207	24.348	1.00	28.96	1DIK2420
ATOM	2329	O	VAL	309	12.050	7.990	24.554	1.00	28.02	1DIK2421
ATOM	2330	CB	VAL	309	9.725	9.692	23.367	1.00	19.99	1DIK2422
ATOM	2331	CG1	VAL	309	9.351	10.630	24.506	1.00	14.96	1DIK2423
ATOM	2332	CG2	VAL	309	8.963	10.053	22.112	1.00	21.23	1DIK2424
ATOM	2333	N	HIS	310	12.480	10.118	25.166	1.00	32.25	1DIK2425
ATOM	2334	CA	HIS	310	13.101	9.751	26.433	1.00	30.63	1DIK2426
ATOM	2335	C	HIS	310	12.270	10.503	27.447	1.00	28.25	1DIK2427
ATOM	2336	O	HIS	310	12.459	11.699	27.668	1.00	29.12	1DIK2428
ATOM	2337	CB	HIS	310	14.573	10.160	26.502	1.00	35.26	1DIK2429
ATOM	2338	CG	HIS	310	15.477	9.219	25.772	1.00	46.85	1DIK2430
ATOM	2339	ND1	HIS	310	15.732	9.329	24.418	1.00	53.75	1DIK2431
ATOM	2340	CD2	HIS	310	16.148	8.117	26.191	1.00	52.66	1DIK2432
ATOM	2341	CE1	HIS	310	16.517	8.339	24.032	1.00	54.18	1DIK2433
ATOM	2342	NE2	HIS	310	16.784	7.588	25.089	1.00	57.76	1DIK2434
ATOM	2343	N	ASP	311	11.326	9.795	28.047	1.00	25.80	1DIK2435
ATOM	2344	CA	ASP	311	10.450	10.404	29.019	1.00	24.79	1DIK2436
ATOM	2345	C	ASP	311	9.947	9.348	29.959	1.00	26.98	1DIK2437
ATOM	2346	O	ASP	311	9.707	8.212	29.564	1.00	29.31	1DIK2438
ATOM	2347	CB	ASP	311	9.257	11.064	28.317	1.00	25.99	1DIK2439
ATOM	2348	CG	ASP	311	8.239	11.619	29.292	1.00	24.92	1DIK2440
ATOM	2349	OD1	ASP	311	8.498	12.703	29.844	1.00	24.37	1DIK2441
ATOM	2350	OD2	ASP	311	7.184	10.982	29.512	1.00	21.07	1DIK2442
ATOM	2351	N	ASP	312	9.779	9.740	31.210	1.00	29.33	1DIK2443
ATOM	2352	CA	ASP	312	9.269	8.849	32.217	1.00	29.81	1DIK2444
ATOM	2353	C	ASP	312	8.262	9.626	33.072	1.00	32.06	1DIK2445
ATOM	2354	O	ASP	312	8.201	9.465	34.294	1.00	33.19	1DIK2446
ATOM	2355	CB	ASP	312	10.422	8.309	33.061	1.00	32.29	1DIK2447
ATOM	2356	CG	ASP	312	10.034	7.062	33.861	1.00	40.96	1DIK2448
ATOM	2357	OD1	ASP	312	8.902	6.523	33.695	1.00	37.90	1DIK2449
ATOM	2358	OD2	ASP	312	10.882	6.616	34.668	1.00	46.83	1DIK2450
ATOM	2359	N	THR	313	7.470	10.475	32.424	1.00	28.45	1DIK2451
ATOM	2360	CA	THR	313	6.472	11.250	33.143	1.00	26.99	1DIK2452
ATOM	2361	C	THR	313	5.040	10.924	32.685	1.00	27.21	1DIK2453
ATOM	2362	O	THR	313	4.455	9.940	33.145	1.00	25.95	1DIK2454
ATOM	2363	CB	THR	313	6.762	12.771	33.043	1.00	27.49	1DIK2455
ATOM	2364	OG1	THR	313	6.694	13.193	31.671	1.00	21.29	1DIK2456
ATOM	2365	CG2	THR	313	8.164	13.075	33.597	1.00	23.59	1DIK2457
ATOM	2366	N	SER	314	4.476	11.726	31.785	1.00	24.25	1DIK2458
ATOM	2367	CA	SER	314	3.105	11.510	31.326	1.00	20.48	1DIK2459
ATOM	2368	C	SER	314	2.936	10.702	30.042	1.00	20.74	1DIK2460
ATOM	2369	O	SER	314	1.821	10.289	29.712	1.00	20.71	1DIK2461
ATOM	2370	CB	SER	314	2.409	12.867	31.160	1.00	20.21	1DIK2462
ATOM	2371	OG	SER	314	3.137	13.722	30.286	1.00	23.16	1DIK2463
ATOM	2372	N	SER	315	4.028	10.468	29.317	1.00	21.85	1DIK2464
ATOM	2373	CA	SER	315	3.923	9.757	28.055	1.00	20.97	1DIK2465
ATOM	2374	C	SER	315	3.568	8.288	28.141	1.00	23.67	1DIK2466
ATOM	2375	O	SER	315	3.890					

Figure 8/30

ATOM	2388	C	HIS	317	5.289	3.406	25.149	1.00	18.22	1DIK2480
ATOM	2389	O	HIS	317	6.015	3.392	24.152	1.00	21.43	1DIK2481
ATOM	2390	CB	HIS	317	6.341	3.401	27.380	1.00	19.52	1DIK2482
ATOM	2391	CG	HIS	317	6.708	4.125	28.640	1.00	25.20	1DIK2483
ATOM	2392	ND1	HIS	317	7.379	5.332	28.643	1.00	28.94	1DIK2484
ATOM	2393	CD2	HIS	317	6.503	3.808	29.940	1.00	26.03	1DIK2485
ATOM	2394	CE1	HIS	317	7.571	5.728	29.888	1.00	27.28	1DIK2486
ATOM	2395	NE2	HIS	317	7.049	4.821	30.694	1.00	31.03	1DIK2487
ATOM	2396	N	THR	318	4.187	2.670	25.255	1.00	18.44	1DIK2488
ATOM	2397	CA	THR	318	3.740	1.800	24.180	1.00	18.99	1DIK2489
ATOM	2398	C	THR	318	3.329	2.644	22.978	1.00	21.41	1DIK2490
ATOM	2399	O	THR	318	3.764	2.399	21.851	1.00	20.04	1DIK2491
ATOM	2400	CB	THR	318	2.544	0.955	24.632	1.00	18.88	1DIK2492
ATOM	2401	OG1	THR	318	2.889	0.310	25.857	1.00	18.06	1DIK2493
ATOM	2402	CG2	THR	318	2.188	-0.116	23.594	1.00	14.25	1DIK2494
ATOM	2403	N	LEU	319	2.500	3.650	23.221	1.00	20.99	1DIK2495
ATOM	2404	CA	LEU	319	2.030	4.509	22.151	1.00	21.53	1DIK2496
ATOM	2405	C	LEU	319	3.171	5.205	21.383	1.00	25.80	1DIK2497
ATOM	2406	O	LEU	319	3.091	5.371	20.165	1.00	25.17	1DIK2498
ATOM	2407	CB	LEU	319	1.085	5.541	22.733	1.00	20.62	1DIK2499
ATOM	2408	CG	LEU	319	0.100	6.148	21.761	1.00	22.28	1DIK2500
ATOM	2409	CD1	LEU	319	-0.686	5.029	21.099	1.00	23.07	1DIK2501
ATOM	2410	CD2	LEU	319	-0.819	7.079	22.522	1.00	20.45	1DIK2502
ATOM	2411	N	ASP	320	4.234	5.603	22.085	1.00	24.35	1DIK2503
ATOM	2412	CA	ASP	320	5.360	6.297	21.445	1.00	22.47	1DIK2504
ATOM	2413	C	ASP	320	6.493	5.459	20.884	1.00	21.00	1DIK2505
ATOM	2414	O	ASP	320	7.437	6.005	20.317	1.00	17.90	1DIK2506
ATOM	2415	CB	ASP	320	5.956	7.325	22.403	1.00	19.58	1DIK2507
ATOM	2416	CG	ASP	320	5.061	8.531	22.582	1.00	22.62	1DIK2508
ATOM	2417	OD1	ASP	320	3.909	8.509	22.092	1.00	22.05	1DIK2509
ATOM	2418	OD2	ASP	320	5.509	9.505	23.214	1.00	18.12	1DIK2510
ATOM	2419	N	SER	321	6.407	4.143	21.024	1.00	22.21	1DIK2511
ATOM	2420	CA	SER	321	7.477	3.271	20.556	1.00	25.24	1DIK2512
ATOM	2421	C	SER	321	7.416	2.869	19.082	1.00	25.75	1DIK2513
ATOM	2422	O	SER	321	8.382	2.315	18.539	1.00	25.63	1DIK2514
ATOM	2423	CB	SER	321	7.496	2.023	21.417	1.00	23.95	1DIK2515
ATOM	2424	OG	SER	321	6.265	1.358	21.278	1.00	33.89	1DIK2516
ATOM	2425	N	SER	322	6.288	3.155	18.441	1.00	27.36	1DIK2517
ATOM	2426	CA	SER	322	6.084	2.776	17.053	1.00	27.84	1DIK2518
ATOM	2427	C	SER	322	5.695	3.928	16.118	1.00	27.85	1DIK2519
ATOM	2428	O	SER	322	4.948	4.838	16.502	1.00	26.35	1DIK2520
ATOM	2429	CB	SER	322	5.016	1.677	17.007	1.00	27.18	1DIK2521
ATOM	2430	OG	SER	322	4.568	1.439	15.688	1.00	34.11	1DIK2522
ATOM	2431	N	PRO	323	6.206	3.895	14.872	1.00	27.40	1DIK2523
ATOM	2432	CA	PRO	323	5.967	4.880	13.807	1.00	27.34	1DIK2524
ATOM	2433	C	PRO	323	4.471	5.053	13.496	1.00	26.66	1DIK2525
ATOM	2434	O	PRO	323	4.037	6.111	13.049	1.00	29.69	1DIK2526
ATOM	2435	CB	PRO	323	6.713	4.276	12.611	1.00	27.47	1DIK2527
ATOM	2436	CG	PRO	323	7.827	3.522	13.251	1.00	26.17	1DIK2528
ATOM	2437	CD	PRO	323	7.121	2.840	14.398	1.00	25.07	1DIK2529
ATOM	2438	N	ALA	324	3.685	4.014	13.732	1.00	23.94	1DIK2530
ATOM	2439	CA	ALA	324	2.258	4.086	13.465	1.00	24.16	1DIK2531
ATOM	2440	C	ALA	324	1.558	5.072	14.381	1.00	21.32	1DIK2532
ATOM	2441	O	ALA	324	0.598	5.712	13.984	1.00	24.85	1DIK2533
ATOM	2442	CB	ALA	324	1.615	2.709	13.615	1.00	23.92	1DIK2534
ATOM	2443	N	THR	325	2.024	5.194	15.612	1.00	19.68	1DIK2535
ATOM	2444	CA	THR	325	1.379	6.097	16.537	1.00	18.15	1DIK2536
ATOM	2445	C	THR	325	2.260	7.256	16.940	1.00	20.32	1DIK2537
ATOM	2446	O	THR	325	1.791	8.183	17.602	1.00	20.91	1DIK2538
ATOM	2447	CB	THR	325	0.898	5.350	17.764	1.00	18.83	1DIK2539
ATOM	2448	OG1	THR	325	1.907	4.428	18.161	1.00	23.06	1DIK2540
ATOM	2449	CG2	THR	325	-0.375	4.579	17.451	1.00	18.83	1DIK2541
ATOM	2450	N	PHE	326	3.532	7.202	16.548	1.00	19.80	1DIK2542
ATOM	2451	CA	PHE	326	4.467	8.282	16.824	1.00	18.01	1DIK2543
ATOM	2452	C	PHE	326	5.605	8.328	15.787	1.00	18.87	1DIK2544
ATOM	2453	O	PHE	326	6.725	7.875	16.046	1.00	20.23	1DIK2545
ATOM	2454	CB	PHE	326	5.024	8.183	18.256	1.00	22.80	1DIK2546
ATOM	2455	CG	PHE	326	5.620	9.478	18.761	1.00	20.42	1DIK2547
ATOM	2456	CD1	PHE	326	4.810	10.445	19.362	1.00	19.30	1DIK2548
ATOM	2457	CD2	PHE	326	6.979	9.755	18.595	1.00	19.81	1DIK2549
ATOM	2458	CE1	PHE	326	5.340	11.680	19.790	1.00	12.22	1DIK2550
ATOM	2459	CE2	PHE	326	7.515	10.984	19.018	1.00	18.58	1DIK2551
ATOM	2460	CZ	PHE	326	6.686	11.948	19.617	1.00	14.93	1DIK2552
ATOM	2461</									

Figure 8/31

ATOM	2473	CG	LEU	328	10.576	9.272	15.625	1.00	25.54	1DIK2565
ATOM	2474	CD1	LEU	328	11.869	8.560	15.990	1.00	24.58	1DIK2566
ATOM	2475	CD2	LEU	328	10.092	10.137	16.782	1.00	22.69	1DIK2567
ATOM	2476	N	ASN	329	9.473	11.220	11.403	1.00	26.61	1DIK2568
ATOM	2477	CA	ASN	329	9.865	11.919	10.198	1.00	29.63	1DIK2569
ATOM	2478	C	ASN	329	8.759	12.578	9.413	1.00	27.72	1DIK2570
ATOM	2479	O	ASN	329	8.941	12.876	8.243	1.00	32.13	1DIK2571
ATOM	2480	CB	ASN	329	10.686	11.001	9.288	1.00	36.18	1DIK2572
ATOM	2481	CG	ASN	329	12.075	10.733	9.843	1.00	48.05	1DIK2573
ATOM	2482	OD1	ASN	329	12.927	11.632	9.873	1.00	52.99	1DIK2574
ATOM	2483	ND2	ASN	329	12.315	9.494	10.290	1.00	53.32	1DIK2575
ATOM	2484	N	SER	330	7.601	12.797	10.020	1.00	28.90	1DIK2576
ATOM	2485	CA	SER	330	6.550	13.530	9.313	1.00	30.10	1DIK2577
ATOM	2486	C	SER	330	7.141	14.938	9.429	1.00	33.67	1DIK2578
ATOM	2487	O	SER	330	8.041	15.193	10.257	1.00	39.71	1DIK2579
ATOM	2488	CB	SER	330	5.212	13.489	10.054	1.00	27.33	1DIK2580
ATOM	2489	OG	SER	330	4.824	12.169	10.372	1.00	30.99	1DIK2581
ATOM	2490	N	THR	331	6.670	15.869	8.633	1.00	29.23	1DIK2582
ATOM	2491	CA	THR	331	7.260	17.198	8.729	1.00	29.49	1DIK2583
ATOM	2492	C	THR	331	6.303	18.150	9.420	1.00	25.32	1DIK2584
ATOM	2493	O	THR	331	6.714	19.147	10.005	1.00	22.51	1DIK2585
ATOM	2494	CB	THR	331	7.590	17.690	7.321	1.00	31.50	1DIK2586
ATOM	2495	OG1	THR	331	8.453	16.737	6.705	1.00	27.95	1DIK2587
ATOM	2496	CG2	THR	331	8.242	19.035	7.343	1.00	36.14	1DIK2588
ATOM	2497	N	LEU	332	5.021	17.804	9.334	1.00	24.55	1DIK2589
ATOM	2498	CA	LEU	332	3.930	18.578	9.885	1.00	23.43	1DIK2590
ATOM	2499	C	LEU	332	3.168	17.760	10.916	1.00	21.17	1DIK2591
ATOM	2500	O	LEU	332	2.814	16.606	10.655	1.00	20.55	1DIK2592
ATOM	2501	CB	LEU	332	2.965	18.972	8.756	1.00	23.10	1DIK2593
ATOM	2502	CG	LEU	332	3.542	19.823	7.625	1.00	25.75	1DIK2594
ATOM	2503	CD1	LEU	332	2.598	19.836	6.431	1.00	21.25	1DIK2595
ATOM	2504	CD2	LEU	332	3.802	21.223	8.145	1.00	19.61	1DIK2596
ATOM	2505	N	TYR	333	2.916	18.361	12.076	1.00	19.69	1DIK2597
ATOM	2506	CA	TYR	333	2.154	17.720	13.152	1.00	17.57	1DIK2598
ATOM	2507	C	TYR	333	1.101	18.691	13.706	1.00	14.59	1DIK2599
ATOM	2508	O	TYR	333	1.304	19.910	13.718	1.00	17.04	1DIK2600
ATOM	2509	CB	TYR	333	3.076	17.317	14.301	1.00	16.40	1DIK2601
ATOM	2510	CG	TYR	333	4.150	16.329	13.944	1.00	15.46	1DIK2602
ATOM	2511	CD1	TYR	333	3.927	14.962	14.058	1.00	16.50	1DIK2603
ATOM	2512	CD2	TYR	333	5.399	16.758	13.519	1.00	15.19	1DIK2604
ATOM	2513	CE1	TYR	333	4.929	14.039	13.758	1.00	19.21	1DIK2605
ATOM	2514	CE2	TYR	333	6.412	15.845	13.214	1.00	19.07	1DIK2606
ATOM	2515	CZ	TYR	333	6.170	14.487	13.338	1.00	20.05	1DIK2607
ATOM	2516	OH	TYR	333	7.165	13.580	13.056	1.00	20.29	1DIK2608
ATOM	2517	N	ALA	334	-0.022	18.154	14.161	1.00	11.62	1DIK2609
ATOM	2518	CA	ALA	334	-1.072	18.971	14.764	1.00	14.11	1DIK2610
ATOM	2519	C	ALA	334	-1.642	18.190	15.952	1.00	17.81	1DIK2611
ATOM	2520	O	ALA	334	-2.001	17.014	15.808	1.00	20.52	1DIK2612
ATOM	2521	CB	ALA	334	-2.169	19.291	13.763	1.00	6.64	1DIK2613
ATOM	2522	N	ASP	335	-1.706	18.842	17.117	1.00	15.89	1DIK2614
ATOM	2523	CA	ASP	335	-2.234	18.234	18.334	1.00	15.85	1DIK2615
ATOM	2524	C	ASP	335	-3.350	19.116	18.877	1.00	19.02	1DIK2616
ATOM	2525	O	ASP	335	-3.261	20.350	18.823	1.00	17.86	1DIK2617
ATOM	2526	CB	ASP	335	-1.126	18.059	19.392	1.00	16.00	1DIK2618
ATOM	2527	CG	ASP	335	-0.099	16.997	19.001	1.00	20.47	1DIK2619
ATOM	2528	OD1	ASP	335	-0.502	15.948	18.466	1.00	22.42	1DIK2620
ATOM	2529	OD2	ASP	335	1.112	17.201	19.224	1.00	20.56	1DIK2621
ATOM	2530	N	PHE	336	-4.402	18.481	19.395	1.00	18.17	1DIK2622
ATOM	2531	CA	PHE	336	-5.543	19.200	19.937	1.00	17.35	1DIK2623
ATOM	2532	C	PHE	336	-5.774	18.839	21.402	1.00	19.88	1DIK2624
ATOM	2533	O	PHE	336	-5.815	17.655	21.776	1.00	19.43	1DIK2625
ATOM	2534	CB	PHE	336	-6.778	18.940	19.066	1.00	17.54	1DIK2626
ATOM	2535	CG	PHE	336	-6.594	19.394	17.655	1.00	14.71	1DIK2627
ATOM	2536	CD1	PHE	336	-5.954	18.577	16.728	1.00	14.86	1DIK2628
ATOM	2537	CD2	PHE	336	-6.978	20.676	17.271	1.00	14.13	1DIK2629
ATOM	2538	CE1	PHE	336	-5.688	19.036	15.434	1.00	19.47	1DIK2630
ATOM	2539	CE2	PHE	336	-6.721	21.148	15.987	1.00	13.80	1DIK2631
ATOM	2540	CZ	PHE	336	-6.072	20.328	15.065	1.00	15.97	1DIK2632
ATOM	2541	N	SER	337	-5.933	19.881	22.219	1.00	16.75	1DIK2633
ATOM	2542	CA	SER	337	-6.096	19.713	23.642	1.00	15.92	1DIK2634
ATOM	2543	C	SER	337	-6.962	20.793	24.331	1.00	17.12	1DIK2635
ATOM	2544	O	SER	337	-7.708	21.549	23.684	1.00	15.10	1DIK2636
ATOM	2545	CB	SER	337	-4					

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ATOM	2558	CA	ASP	339	-6.436	25.120	27.983	1.00	19.43	1DIK2650
ATOM	2559	C	ASP	339	-5.452	24.739	29.079	1.00	18.53	1DIK2651
ATOM	2560	O	ASP	339	-4.301	25.170	29.052	1.00	22.28	1DIK2652
ATOM	2561	CB	ASP	339	-7.364	26.275	28.452	1.00	23.01	1DIK2653
ATOM	2562	CG	ASP	339	-8.397	25.856	29.528	1.00	25.24	1DIK2654
ATOM	2563	OD1	ASP	339	-8.560	24.654	29.838	1.00	27.53	1DIK2655
ATOM	2564	OD2	ASP	339	-9.066	26.759	30.075	1.00	27.85	1DIK2656
ATOM	2565	N	ASN	340	-5.892	23.922	30.032	1.00	16.85	1DIK2657
ATOM	2566	CA	ASN	340	-5.035	23.514	31.141	1.00	17.73	1DIK2658
ATOM	2567	C	ASN	340	-3.750	22.830	30.712	1.00	19.02	1DIK2659
ATOM	2568	O	ASN	340	-2.666	23.210	31.161	1.00	21.77	1DIK2660
ATOM	2569	CB	ASN	340	-5.810	22.643	32.111	1.00	19.49	1DIK2661
ATOM	2570	CG	ASN	340	-6.815	23.443	32.908	1.00	22.56	1DIK2662
ATOM	2571	OD1	ASN	340	-6.752	24.662	32.945	1.00	25.09	1DIK2663
ATOM	2572	ND2	ASN	340	-7.743	22.762	33.552	1.00	28.53	1DIK2664
ATOM	2573	N	GLY	341	-3.858	21.831	29.845	1.00	17.89	1DIK2665
ATOM	2574	CA	GLY	341	-2.665	21.160	29.364	1.00	15.63	1DIK2666
ATOM	2575	C	GLY	341	-1.764	22.118	28.600	1.00	11.99	1DIK2667
ATOM	2576	O	GLY	341	-0.549	22.077	28.735	1.00	16.11	1DIK2668
ATOM	2577	N	ILE	342	-2.344	22.996	27.797	1.00	13.11	1DIK2669
ATOM	2578	CA	ILE	342	-1.525	23.941	27.036	1.00	17.14	1DIK2670
ATOM	2579	C	ILE	342	-0.755	24.910	27.946	1.00	17.23	1DIK2671
ATOM	2580	O	ILE	342	0.410	25.214	27.694	1.00	17.60	1DIK2672
ATOM	2581	CB	ILE	342	-2.399	24.690	25.990	1.00	16.48	1DIK2673
ATOM	2582	CG1	ILE	342	-2.982	23.663	25.015	1.00	11.17	1DIK2674
ATOM	2583	CG2	ILE	342	-1.574	25.710	25.221	1.00	12.60	1DIK2675
ATOM	2584	CD1	ILE	342	-4.052	24.199	24.138	1.00	14.25	1DIK2676
ATOM	2585	N	ILE	343	-1.397	25.384	29.010	1.00	20.72	1DIK2677
ATOM	2586	CA	ILE	343	-0.747	26.296	29.948	1.00	20.28	1DIK2678
ATOM	2587	C	ILE	343	0.531	25.647	30.503	1.00	21.94	1DIK2679
ATOM	2588	O	ILE	343	1.617	26.243	30.467	1.00	23.12	1DIK2680
ATOM	2589	CB	ILE	343	-1.703	26.677	31.124	1.00	17.08	1DIK2681
ATOM	2590	CG1	ILE	343	-2.757	27.671	30.638	1.00	12.06	1DIK2682
ATOM	2591	CG2	ILE	343	-0.911	27.321	32.277	1.00	12.92	1DIK2683
ATOM	2592	CD1	ILE	343	-2.152	29.042	30.271	1.00	11.66	1DIK2684
ATOM	2593	N	SER	344	0.394	24.424	31.006	1.00	20.30	1DIK2685
ATOM	2594	CA	SER	344	1.519	23.690	31.564	1.00	17.86	1DIK2686
ATOM	2595	C	SER	344	2.636	23.482	30.544	1.00	20.31	1DIK2687
ATOM	2596	O	SER	344	3.825	23.604	30.881	1.00	19.02	1DIK2688
ATOM	2597	CB	SER	344	1.036	22.344	32.081	1.00	18.82	1DIK2689
ATOM	2598	OG	SER	344	0.137	22.512	33.164	1.00	19.78	1DIK2690
ATOM	2599	N	ILE	345	2.248	23.170	29.302	1.00	19.86	1DIK2691
ATOM	2600	CA	ILE	345	3.194	22.940	28.205	1.00	19.61	1DIK2692
ATOM	2601	C	ILE	345	3.990	24.211	27.877	1.00	22.16	1DIK2693
ATOM	2602	O	ILE	345	5.211	24.156	27.678	1.00	21.36	1DIK2694
ATOM	2603	CB	ILE	345	2.460	22.420	26.936	1.00	17.67	1DIK2695
ATOM	2604	CG1	ILE	345	1.926	21.009	27.194	1.00	17.47	1DIK2696
ATOM	2605	CG2	ILE	345	3.389	22.402	25.738	1.00	10.81	1DIK2697
ATOM	2606	CD1	ILE	345	1.129	20.443	26.052	1.00	20.20	1DIK2698
ATOM	2607	N	LEU	346	3.290	25.347	27.828	1.00	21.51	1DIK2699
ATOM	2608	CA	LEU	346	3.906	26.645	27.558	1.00	21.18	1DIK2700
ATOM	2609	C	LEU	346	4.987	26.936	28.610	1.00	19.82	1DIK2701
ATOM	2610	O	LEU	346	6.078	27.401	28.281	1.00	22.60	1DIK2702
ATOM	2611	CB	LEU	346	2.838	27.754	27.559	1.00	21.21	1DIK2703
ATOM	2612	CG	LEU	346	1.787	27.761	26.430	1.00	25.27	1DIK2704
ATOM	2613	CD1	LEU	346	0.797	28.905	26.655	1.00	22.27	1DIK2705
ATOM	2614	CD2	LEU	346	2.457	27.910	25.067	1.00	19.78	1DIK2706
ATOM	2615	N	PHE	347	4.694	26.658	29.875	1.00	21.86	1DIK2707
ATOM	2616	CA	PHE	347	5.679	26.878	30.929	1.00	21.46	1DIK2708
ATOM	2617	C	PHE	347	6.825	25.881	30.884	1.00	24.47	1DIK2709
ATOM	2618	O	PHE	347	7.981	26.282	31.064	1.00	23.78	1DIK2710
ATOM	2619	CB	PHE	347	5.006	26.903	32.300	1.00	22.55	1DIK2711
ATOM	2620	CG	PHE	347	4.289	28.189	32.566	1.00	19.15	1DIK2712
ATOM	2621	CD1	PHE	347	4.977	29.283	33.088	1.00	19.76	1DIK2713
ATOM	2622	CD2	PHE	347	2.953	28.332	32.233	1.00	17.59	1DIK2714
ATOM	2623	CE1	PHE	347	4.341	30.508	33.268	1.00	18.90	1DIK2715
ATOM	2624	CE2	PHE	347	2.311	29.542	32.407	1.00	21.97	1DIK2716
ATOM	2625	CZ	PHE	347	3.007	30.638	32.926	1.00	20.72	1DIK2717
ATOM	2626	N	ALA	348	6.517	24.599	30.634	1.00	25.00	1DIK2718
ATOM	2627	CA	ALA	348	7.547	23.551	30.533	1.00	23.63	1DIK2719
ATOM	2628	C	ALA	348	8.523	23.830	29.374	1.00	23.94	1DIK2720
ATOM	2629	O	ALA	348	9.647	23.327	29.368	1.00	22.81	1DIK2721
ATOM	2630	CB	ALA	348						

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ATOM	2643	N	LEU	351	8.830	29.292	27.997	1.00	31.09	1DIK2735
ATOM	2644	CA	LEU	351	8.367	30.486	27.301	1.00	29.39	1DIK2736
ATOM	2645	C	LEU	351	8.048	31.700	28.184	1.00	30.29	1DIK2737
ATOM	2646	O	LEU	351	8.092	32.841	27.722	1.00	28.55	1DIK2738
ATOM	2647	CB	LEU	351	7.147	30.132	26.456	1.00	31.14	1DIK2739
ATOM	2648	CG	LEU	351	7.359	28.989	25.467	1.00	29.30	1DIK2740
ATOM	2649	CD1	LEU	351	6.063	28.718	24.722	1.00	28.64	1DIK2741
ATOM	2650	CD2	LEU	351	8.483	29.347	24.501	1.00	25.72	1DIK2742
ATOM	2651	N	TYR	352	7.731	31.474	29.453	1.00	31.04	1DIK2743
ATOM	2652	CA	TYR	352	7.410	32.594	30.325	1.00	31.74	1DIK2744
ATOM	2653	C	TYR	352	8.350	32.747	31.502	1.00	34.72	1DIK2745
ATOM	2654	O	TYR	352	7.942	33.102	32.613	1.00	33.44	1DIK2746
ATOM	2655	CB	TYR	352	5.953	32.484	30.752	1.00	26.97	1DIK2747
ATOM	2656	CG	TYR	352	5.090	32.667	29.552	1.00	28.46	1DIK2748
ATOM	2657	CD1	TYR	352	4.916	33.932	29.003	1.00	27.92	1DIK2749
ATOM	2658	CD2	TYR	352	4.506	31.574	28.910	1.00	29.60	1DIK2750
ATOM	2659	CE1	TYR	352	4.190	34.118	27.846	1.00	30.02	1DIK2751
ATOM	2660	CE2	TYR	352	3.773	31.745	27.745	1.00	30.26	1DIK2752
ATOM	2661	C2	TYR	352	3.622	33.029	27.220	1.00	32.93	1DIK2753
ATOM	2662	OH	TYR	352	2.903	33.228	26.067	1.00	33.54	1DIK2754
ATOM	2663	N	ASN	353	9.626	32.484	31.236	1.00	40.74	1DIK2755
ATOM	2664	CA	ASN	353	10.669	32.582	32.251	1.00	47.39	1DIK2756
ATOM	2665	C	ASN	353	10.941	34.011	32.729	1.00	47.72	1DIK2757
ATOM	2666	O	ASN	353	11.505	34.206	33.802	1.00	46.72	1DIK2758
ATOM	2667	CB	ASN	353	11.966	31.932	31.749	1.00	49.39	1DIK2759
ATOM	2668	CG	ASN	353	11.931	30.406	31.832	1.00	51.90	1DIK2760
ATOM	2669	OD1	ASN	353	10.895	29.801	32.155	1.00	51.32	1DIK2761
ATOM	2670	ND2	ASN	353	13.071	29.774	31.537	1.00	57.79	1DIK2762
ATOM	2671	N	GLY	354	10.535	35.002	31.937	1.00	48.40	1DIK2763
ATOM	2672	CA	GLY	354	10.741	36.390	32.319	1.00	49.75	1DIK2764
ATOM	2673	C	GLY	354	9.531	36.974	33.032	1.00	49.81	1DIK2765
ATOM	2674	O	GLY	354	9.424	38.193	33.203	1.00	55.38	1DIK2766
ATOM	2675	N	THR	355	8.622	36.101	33.449	1.00	46.75	1DIK2767
ATOM	2676	CA	THR	355	7.396	36.496	34.135	1.00	46.22	1DIK2768
ATOM	2677	C	THR	355	7.536	36.191	35.631	1.00	47.74	1DIK2769
ATOM	2678	O	THR	355	7.789	35.042	36.007	1.00	47.46	1DIK2770
ATOM	2679	CB	THR	355	6.180	35.691	33.556	1.00	42.82	1DIK2771
ATOM	2680	OG1	THR	355	6.147	35.847	32.131	1.00	43.08	1DIK2772
ATOM	2681	CG2	THR	355	4.853	36.160	34.154	1.00	35.74	1DIK2773
ATOM	2682	N	LYS	356	7.388	37.202	36.486	1.00	44.73	1DIK2774
ATOM	2683	CA	LYS	356	7.478	36.960	37.926	1.00	42.43	1DIK2775
ATOM	2684	C	LYS	356	6.116	36.530	38.437	1.00	40.86	1DIK2776
ATOM	2685	O	LYS	356	5.103	36.849	37.813	1.00	42.40	1DIK2777
ATOM	2686	CB	LYS	356	7.942	38.210	38.664	1.00	41.47	1DIK2778
ATOM	2687	CG	LYS	356	9.438	38.349	38.668	1.00	42.08	1DIK2779
ATOM	2688	CD	LYS	356	9.866	39.579	39.406	1.00	42.64	1DIK2780
ATOM	2689	CE	LYS	356	11.351	39.719	39.346	1.00	42.34	1DIK2781
ATOM	2690	NZ	LYS	356	11.693	41.124	39.631	1.00	48.71	1DIK2782
ATOM	2691	N	PRO	357	6.069	35.806	39.577	1.00	38.87	1DIK2783
ATOM	2692	CA	PRO	357	4.777	35.358	40.120	1.00	39.88	1DIK2784
ATOM	2693	C	PRO	357	3.771	36.512	40.134	1.00	42.03	1DIK2785
ATOM	2694	O	PRO	357	4.092	37.629	40.564	1.00	44.16	1DIK2786
ATOM	2695	CB	PRO	357	5.149	34.869	41.517	1.00	38.17	1DIK2787
ATOM	2696	CG	PRO	357	6.526	34.306	41.295	1.00	34.95	1DIK2788
ATOM	2697	CD	PRO	357	7.183	35.366	40.438	1.00	33.26	1DIK2789
ATOM	2698	N	LEU	358	2.562	36.252	39.649	1.00	40.53	1DIK2790
ATOM	2699	CA	LEU	358	1.555	37.298	39.584	1.00	39.23	1DIK2791
ATOM	2700	C	LEU	358	1.075	37.682	40.975	1.00	40.76	1DIK2792
ATOM	2701	O	LEU	358	0.861	36.815	41.821	1.00	40.81	1DIK2793
ATOM	2702	CB	LEU	358	0.355	36.864	38.732	1.00	37.58	1DIK2794
ATOM	2703	CG	LEU	358	0.499	36.397	37.283	1.00	34.63	1DIK2795
ATOM	2704	CD1	LEU	358	-0.862	36.528	36.631	1.00	32.21	1DIK2796
ATOM	2705	CD2	LEU	358	1.512	37.210	36.528	1.00	33.59	1DIK2797
ATOM	2706	N	SER	359	0.900	38.979	41.205	1.00	39.69	1DIK2798
ATOM	2707	CA	SER	359	0.432	39.461	42.494	1.00	40.29	1DIK2799
ATOM	2708	C	SER	359	-0.963	38.910	42.687	1.00	38.32	1DIK2800
ATOM	2709	O	SER	359	-1.763	38.923	41.758	1.00	38.66	1DIK2801
ATOM	2710	CB	SER	359	0.376	40.989	42.515	1.00	43.59	1DIK2802
ATOM	2711	OG	SER	359	-0.234	41.445	43.720	1.00	51.02	1DIK2803
ATOM	2712	N	THR	360	-1.254	38.432	43.889	1.00	37.92	1DIK2804
ATOM	2713	CA	THR	360	-2.564	37.870	44.189	1.00	40.16	1DIK2805
ATOM	2714	C	THR	360	-3.564	38.907	44.709	1.00	39.58	1DIK2806

Figure 8/34

ATOM	2728	C	THR	362	-3.134	43.247	41.138	1.00	42.73	1DIK2820
ATOM	2729	O	THR	362	-2.368	42.332	40.846	1.00	43.39	1DIK2821
ATOM	2730	CB	THR	362	-2.142	44.689	42.867	1.00	49.03	1DIK2822
ATOM	2731	OG1	THR	362	-2.006	44.846	44.287	1.00	56.76	1DIK2823
ATOM	2732	CG2	THR	362	-2.434	46.036	42.227	1.00	50.37	1DIK2824
ATOM	2733	N	VAL	363	-3.879	43.901	40.249	1.00	40.72	1DIK2825
ATOM	2734	CA	VAL	363	-3.860	43.616	38.815	1.00	37.30	1DIK2826
ATOM	2735	C	VAL	363	-2.524	44.081	38.243	1.00	39.07	1DIK2827
ATOM	2736	O	VAL	363	-2.045	45.160	38.603	1.00	40.33	1DIK2828
ATOM	2737	CB	VAL	363	-4.982	44.402	38.070	1.00	34.35	1DIK2829
ATOM	2738	CG1	VAL	363	-4.928	44.143	36.562	1.00	33.50	1DIK2830
ATOM	2739	CG2	VAL	363	-6.332	44.034	38.625	1.00	32.51	1DIK2831
ATOM	2740	N	GLU	364	-1.934	43.269	37.366	1.00	38.65	1DIK2832
ATOM	2741	CA	GLU	364	-0.676	43.602	36.694	1.00	40.15	1DIK2833
ATOM	2742	C	GLU	364	-0.961	43.550	35.199	1.00	41.61	1DIK2834
ATOM	2743	O	GLU	364	-1.619	42.628	34.714	1.00	42.19	1DIK2835
ATOM	2744	CB	GLU	364	0.421	42.606	37.040	1.00	39.16	1DIK2836
ATOM	2745	CG	GLU	364	0.621	42.449	38.515	1.00	45.46	1DIK2837
ATOM	2746	CD	GLU	364	1.956	41.863	38.842	1.00	46.24	1DIK2838
ATOM	2747	OE1	GLU	364	2.953	42.609	38.751	1.00	54.58	1DIK2839
ATOM	2748	OE2	GLU	364	2.013	40.666	39.187	1.00	43.12	1DIK2840
ATOM	2749	N	ASN	365	-0.475	44.540	34.466	1.00	41.88	1DIK2841
ATOM	2750	CA	ASN	365	-0.727	44.587	33.037	1.00	41.03	1DIK2842
ATOM	2751	C	ASN	365	0.218	43.661	32.288	1.00	39.55	1DIK2843
ATOM	2752	O	ASN	365	1.181	43.141	32.866	1.00	34.92	1DIK2844
ATOM	2753	CB	ASN	365	-0.615	46.025	32.513	1.00	46.26	1DIK2845
ATOM	2754	CG	ASN	365	0.786	46.589	32.649	1.00	49.70	1DIK2846
ATOM	2755	OD1	ASN	365	1.646	46.361	31.798	1.00	52.55	1DIK2847
ATOM	2756	ND2	ASN	365	1.024	47.323	33.719	1.00	56.03	1DIK2848
ATOM	2757	N	ILE	366	-0.075	43.481	30.999	1.00	38.20	1DIK2849
ATOM	2758	CA	ILE	366	0.671	42.603	30.103	1.00	36.15	1DIK2850
ATOM	2759	C	ILE	366	2.160	42.944	29.939	1.00	37.55	1DIK2851
ATOM	2760	O	ILE	366	2.947	42.107	29.489	1.00	38.87	1DIK2852
ATOM	2761	CB	ILE	366	-0.068	42.489	28.713	1.00	33.38	1DIK2853
ATOM	2762	CG1	ILE	366	0.239	41.136	28.084	1.00	29.94	1DIK2854
ATOM	2763	CG2	ILE	366	0.273	43.652	27.786	1.00	24.77	1DIK2855
ATOM	2764	CD1	ILE	366	-0.332	39.987	28.874	1.00	22.62	1DIK2856
ATOM	2765	N	THR	367	2.542	44.165	30.302	1.00	37.95	1DIK2857
ATOM	2766	CA	THR	367	3.944	44.592	30.243	1.00	40.36	1DIK2858
ATOM	2767	C	THR	367	4.654	44.030	31.486	1.00	40.59	1DIK2859
ATOM	2768	O	THR	367	5.775	43.512	31.406	1.00	40.36	1DIK2860
ATOM	2769	CB	THR	367	4.058	46.149	30.248	1.00	41.59	1DIK2861
ATOM	2770	OG1	THR	367	3.625	46.663	28.983	1.00	38.58	1DIK2862
ATOM	2771	CG2	THR	367	5.488	46.602	30.535	1.00	43.44	1DIK2863
ATOM	2772	N	GLN	368	3.985	44.135	32.630	1.00	39.60	1DIK2864
ATOM	2773	CA	GLN	368	4.532	43.647	33.880	1.00	42.39	1DIK2865
ATOM	2774	C	GLN	368	4.656	42.133	33.876	1.00	43.99	1DIK2866
ATOM	2775	O	GLN	368	5.613	41.598	34.438	1.00	47.07	1DIK2867
ATOM	2776	CB	GLN	368	3.650	44.055	35.050	1.00	46.02	1DIK2868
ATOM	2777	CG	GLN	368	3.575	45.543	35.313	1.00	52.12	1DIK2869
ATOM	2778	CD	GLN	368	2.605	45.854	36.439	1.00	55.80	1DIK2870
ATOM	2779	OE1	GLN	368	1.553	46.460	36.223	1.00	53.21	1DIK2871
ATOM	2780	NZ2	GLN	368	2.953	45.432	37.649	1.00	58.79	1DIK2872
ATOM	2781	N	THR	369	3.691	41.447	33.250	1.00	42.31	1DIK2873
ATOM	2782	CA	THR	369	3.691	39.980	33.195	1.00	37.86	1DIK2874
ATOM	2783	C	THR	369	4.457	39.399	32.018	1.00	35.95	1DIK2875
ATOM	2784	O	THR	369	4.415	38.186	31.776	1.00	32.63	1DIK2876
ATOM	2785	CB	THR	369	2.273	39.404	33.156	1.00	37.12	1DIK2877
ATOM	2786	OG1	THR	369	1.626	39.815	31.940	1.00	40.70	1DIK2878
ATOM	2787	CG2	THR	369	1.475	39.871	34.368	1.00	28.31	1DIK2879
ATOM	2788	N	ASP	370	5.149	40.269	31.291	1.00	33.39	1DIK2880
ATOM	2789	CA	ASP	370	5.954	39.864	30.153	1.00	32.87	1DIK2881
ATOM	2790	C	ASP	370	5.170	39.043	29.104	1.00	31.05	1DIK2882
ATOM	2791	O	ASP	370	5.608	37.979	28.656	1.00	31.02	1DIK2883
ATOM	2792	CB	ASP	370	7.191	39.099	30.655	1.00	35.44	1DIK2884
ATOM	2793	CG	ASP	370	8.319	39.065	29.629	1.00	40.37	1DIK2885
ATOM	2794	OD1	ASP	370	8.469	40.065	28.893	1.00	35.88	1DIK2886
ATOM	2795	OD2	ASP	370	9.052	38.043	29.558	1.00	39.79	1DIK2887
ATOM	2796	N	GLY	371	4.003	39.548	28.721	1.00	29.15	1DIK2888
ATOM	2797	CA	GLY	371	3.203	38.883	27.717	1.00	26.42	1DIK2889
ATOM	2798	C	GLY	371	2.322	37.745	28.178	1.00	29.16	1DIK2890
ATOM	2799	O	GLY	371	1.686	37.105	27.350	1.00	31.15	1DIK2891
ATOM	2800	N	PHE							

Figure 8/35

ATOM	2813	C	SER	373	-3.191	35.201	29.772	1.00	25.82	1DIK2905
ATOM	2814	O	SER	373	-2.776	34.638	28.753	1.00	26.67	1DIK2906
ATOM	2815	CB	SER	373	-2.945	37.716	29.914	1.00	20.86	1DIK2907
ATOM	2816	OG	SER	373	-3.520	37.661	28.620	1.00	26.28	1DIK2908
ATOM	2817	N	SER	374	-4.310	34.820	30.378	1.00	23.66	1DIK2909
ATOM	2818	CA	SER	374	-5.092	33.728	29.816	1.00	23.58	1DIK2910
ATOM	2819	C	SER	374	-5.576	34.063	28.418	1.00	21.38	1DIK2911
ATOM	2820	O	SER	374	-5.596	33.201	27.552	1.00	24.01	1DIK2912
ATOM	2821	CB	SER	374	-6.295	33.404	30.688	1.00	24.78	1DIK2913
ATOM	2822	OG	SER	374	-5.868	32.729	31.846	1.00	36.24	1DIK2914
ATOM	2823	N	ALA	375	-5.965	35.316	28.209	1.00	19.17	1DIK2915
ATOM	2824	CA	ALA	375	-6.462	35.774	26.919	1.00	18.77	1DIK2916
ATOM	2825	C	ALA	375	-5.377	35.768	25.839	1.00	19.10	1DIK2917
ATOM	2826	O	ALA	375	-5.674	35.603	24.662	1.00	17.13	1DIK2918
ATOM	2827	CB	ALA	375	-7.066	37.176	27.060	1.00	17.12	1DIK2919
ATOM	2828	N	TRP	376	-4.124	35.948	26.241	1.00	18.21	1DIK2920
ATOM	2829	CA	TRP	376	-3.028	35.956	25.285	1.00	20.78	1DIK2921
ATOM	2830	C	TRP	376	-2.419	34.585	25.036	1.00	22.76	1DIK2922
ATOM	2831	O	TRP	376	-1.724	34.391	24.032	1.00	24.41	1DIK2923
ATOM	2832	CB	TRP	376	-1.922	36.932	25.720	1.00	20.50	1DIK2924
ATOM	2833	CG	TRP	376	-2.236	38.359	25.406	1.00	21.91	1DIK2925
ATOM	2834	CD1	TRP	376	-3.465	38.941	25.432	1.00	21.75	1DIK2926
ATOM	2835	CD2	TRP	376	-1.309	39.389	25.017	1.00	23.53	1DIK2927
ATOM	2836	NE1	TRP	376	-3.368	40.265	25.085	1.00	23.80	1DIK2928
ATOM	2837	CE2	TRP	376	-2.060	40.572	24.824	1.00	24.79	1DIK2929
ATOM	2838	CE3	TRP	376	0.082	39.429	24.814	1.00	26.46	1DIK2930
ATOM	2839	CZ2	TRP	376	-1.468	41.794	24.435	1.00	25.72	1DIK2931
ATOM	2840	CZ3	TRP	376	0.676	40.649	24.425	1.00	24.82	1DIK2932
ATOM	2841	CH2	TRP	376	-0.106	41.812	24.242	1.00	24.72	1DIK2933
ATOM	2842	N	THR	377	-2.670	33.631	25.931	1.00	23.05	1DIK2934
ATOM	2843	CA	THR	377	-2.105	32.296	25.770	1.00	20.73	1DIK2935
ATOM	2844	C	THR	377	-3.128	31.212	25.438	1.00	21.78	1DIK2936
ATOM	2845	O	THR	377	-2.917	30.422	24.499	1.00	22.28	1DIK2937
ATOM	2846	CB	THR	377	-1.282	31.891	27.015	1.00	21.05	1DIK2938
ATOM	2847	OG1	THR	377	-2.125	31.885	28.181	1.00	20.07	1DIK2939
ATOM	2848	CG2	THR	377	-0.122	32.871	27.215	1.00	17.56	1DIK2940
ATOM	2849	N	VAL	378	-4.232	31.177	26.187	1.00	19.66	1DIK2941
ATOM	2850	CA	VAL	378	-5.266	30.173	25.960	1.00	17.69	1DIK2942
ATOM	2851	C	VAL	378	-6.712	30.611	25.663	1.00	19.05	1DIK2943
ATOM	2852	O	VAL	378	-7.657	30.160	26.323	1.00	18.97	1DIK2944
ATOM	2853	CB	VAL	378	-5.290	29.124	27.103	1.00	19.46	1DIK2945
ATOM	2854	CG1	VAL	378	-4.018	28.291	27.061	1.00	16.35	1DIK2946
ATOM	2855	CG2	VAL	378	-5.461	29.811	28.459	1.00	17.47	1DIK2947
ATOM	2856	N	PRO	379	-6.909	31.510	24.681	1.00	19.03	1DIK2948
ATOM	2857	CA	PRO	379	-8.300	31.878	24.405	1.00	17.80	1DIK2949
ATOM	2858	C	PRO	379	-8.910	30.654	23.696	1.00	19.39	1DIK2950
ATOM	2859	O	PRO	379	-8.215	29.655	23.472	1.00	21.31	1DIK2951
ATOM	2860	CB	PRO	379	-8.149	33.045	23.438	1.00	16.10	1DIK2952
ATOM	2861	CG	PRO	379	-6.877	32.691	22.677	1.00	17.21	1DIK2953
ATOM	2862	CD	PRO	379	-5.979	32.249	23.798	1.00	19.06	1DIK2954
ATOM	2863	N	PHE	380	-10.188	30.704	23.344	1.00	18.52	1DIK2955
ATOM	2864	CA	PHE	380	-10.784	29.588	22.608	1.00	18.85	1DIK2956
ATOM	2865	C	PHE	380	-10.052	29.506	21.263	1.00	21.10	1DIK2957
ATOM	2866	O	PHE	380	-9.733	30.535	20.669	1.00	24.26	1DIK2958
ATOM	2867	CB	PHE	380	-12.260	29.843	22.329	1.00	17.78	1DIK2959
ATOM	2868	CG	PHE	380	-13.150	29.637	23.509	1.00	20.97	1DIK2960
ATOM	2869	CD1	PHE	380	-13.089	28.461	24.247	1.00	18.51	1DIK2961
ATOM	2870	CD2	PHE	380	-14.084	30.615	23.868	1.00	22.13	1DIK2962
ATOM	2871	CE1	PHE	380	-13.945	28.252	25.327	1.00	23.16	1DIK2963
ATOM	2872	CE2	PHE	380	-14.942	30.419	24.941	1.00	20.92	1DIK2964
ATOM	2873	CZ	PHE	380	-14.874	29.229	25.677	1.00	18.80	1DIK2965
ATOM	2874	N	ALA	381	-9.790	28.296	20.785	1.00	19.83	1DIK2966
ATOM	2875	CA	ALA	381	-9.106	28.103	19.514	1.00	17.83	1DIK2967
ATOM	2876	C	ALA	381	-7.703	28.731	19.476	1.00	21.42	1DIK2968
ATOM	2877	O	ALA	381	-7.225	29.148	18.414	1.00	23.62	1DIK2969
ATOM	2878	CB	ALA	381	-9.968	28.641	18.369	1.00	16.06	1DIK2970
ATOM	2879	N	SER	382	-7.035	28.809	20.622	1.00	16.01	1DIK2971
ATOM	2880	CA	SER	382	-5.699	29.359	20.625	1.00	16.41	1DIK2972
ATOM	2881	C	SER	382	-4.814	28.403	19.850	1.00	16.99	1DIK2973
ATOM	2882	O	SER	382	-5.165	27.240	19.674	1.00	21.80	1DIK2974
ATOM	2883	CB	SER	382	-5.170	29.462	22.046	1.00	18.69	1DIK2975
ATOM	2884	OG	SER	382	-5.083	28.174	22.612	1.00	19.41	1DIK2976
ATOM	2885	N	ARG</							

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ATOM	2898	C	LEU	384	1.632	26.976	18.156	1.00	17.51	1DIK2990
ATOM	2899	O	LEU	384	1.239	25.859	17.776	1.00	17.66	1DIK2991
ATOM	2900	CB	LEU	384	1.384	26.904	20.641	1.00	14.47	1DIK2992
ATOM	2901	CG	LEU	384	2.834	26.416	20.797	1.00	23.97	1DIK2993
ATOM	2902	CD1	LEU	384	3.761	27.555	21.205	1.00	22.30	1DIK2994
ATOM	2903	CD2	LEU	384	2.880	25.312	21.859	1.00	26.10	1DIK2995
ATOM	2904	N	TYR	385	2.601	27.658	17.546	1.00	17.61	1DIK2996
ATOM	2905	CA	TYR	385	3.336	27.110	16.402	1.00	14.96	1DIK2997
ATOM	2906	C	TYR	385	4.794	26.962	16.803	1.00	17.08	1DIK2998
ATOM	2907	O	TYR	385	5.379	27.860	17.428	1.00	15.24	1DIK2999
ATOM	2908	CB	TYR	385	3.341	28.047	15.186	1.00	12.27	1DIK3000
ATOM	2909	CG	TYR	385	2.021	28.338	14.532	1.00	14.64	1DIK3001
ATOM	2910	CD1	TYR	385	1.004	27.383	14.479	1.00	15.16	1DIK3002
ATOM	2911	CD2	TYR	385	1.795	29.580	13.942	1.00	17.04	1DIK3003
ATOM	2912	CE1	TYR	385	-0.209	27.657	13.854	1.00	16.98	1DIK3004
ATOM	2913	CE2	TYR	385	0.584	29.870	13.309	1.00	18.46	1DIK3005
ATOM	2914	C2	TYR	385	-0.418	28.910	13.265	1.00	21.91	1DIK3006
ATOM	2915	OH	TYR	385	-1.620	29.216	12.637	1.00	13.55	1DIK3007
ATOM	2916	N	VAL	386	5.381	25.829	16.448	1.00	18.39	1DIK3008
ATOM	2917	CA	VAL	386	6.793	25.606	16.681	1.00	16.56	1DIK3009
ATOM	2918	C	VAL	386	7.285	25.311	15.279	1.00	17.90	1DIK3010
ATOM	2919	O	VAL	386	6.893	24.298	14.680	1.00	20.76	1DIK3011
ATOM	2920	CB	VAL	386	7.067	24.404	17.577	1.00	16.14	1DIK3012
ATOM	2921	CG1	VAL	386	8.572	24.270	17.787	1.00	6.88	1DIK3013
ATOM	2922	CG2	VAL	386	6.346	24.565	18.910	1.00	15.11	1DIK3014
ATOM	2923	N	GLU	387	8.116	26.198	14.745	1.00	17.38	1DIK3015
ATOM	2924	CA	GLU	387	8.656	26.029	13.400	1.00	19.62	1DIK3016
ATOM	2925	C	GLU	387	10.169	25.935	13.407	1.00	19.53	1DIK3017
ATOM	2926	O	GLU	387	10.834	26.508	14.269	1.00	21.49	1DIK3018
ATOM	2927	CB	GLU	387	8.211	27.185	12.488	1.00	19.65	1DIK3019
ATOM	2928	CG	GLU	387	8.456	28.572	13.064	1.00	24.89	1DIK3020
ATOM	2929	CD	GLU	387	7.839	29.707	12.237	1.00	25.32	1DIK3021
ATOM	2930	OE1	GLU	387	6.675	29.590	11.802	1.00	18.28	1DIK3022
ATOM	2931	OE2	GLU	387	8.531	30.726	12.030	1.00	24.15	1DIK3023
ATOM	2932	N	MET	388	10.708	25.196	12.448	1.00	22.89	1DIK3024
ATOM	2933	CA	MET	388	12.148	25.047	12.306	1.00	24.50	1DIK3025
ATOM	2934	C	MET	388	12.420	25.506	10.872	1.00	25.97	1DIK3026
ATOM	2935	O	MET	388	11.629	25.226	9.962	1.00	24.86	1DIK3027
ATOM	2936	CB	MET	388	12.564	23.596	12.542	1.00	24.86	1DIK3028
ATOM	2937	CG	MET	388	14.045	23.405	12.736	1.00	28.49	1DIK3029
ATOM	2938	SD	MET	388	14.420	21.945	13.737	1.00	32.00	1DIK3030
ATOM	2939	CE	MET	388	13.569	20.648	12.835	1.00	25.36	1DIK3031
ATOM	2940	N	MET	389	13.517	26.233	10.673	1.00	26.04	1DIK3032
ATOM	2941	CA	MET	389	13.863	26.749	9.351	1.00	27.38	1DIK3033
ATOM	2942	C	MET	389	15.354	26.673	9.063	1.00	31.05	1DIK3034
ATOM	2943	O	MET	389	16.186	26.532	9.970	1.00	28.80	1DIK3035
ATOM	2944	CB	MET	389	13.388	28.200	9.188	1.00	21.65	1DIK3036
ATOM	2945	CG	MET	389	13.986	29.170	10.190	1.00	20.31	1DIK3037
ATOM	2946	SD	MET	389	13.301	30.826	10.047	1.00	27.29	1DIK3038
ATOM	2947	CE	MET	389	11.760	30.668	10.980	1.00	23.61	1DIK3039
ATOM	2948	N	GLN	390	15.683	26.752	7.782	1.00	33.50	1DIK3040
ATOM	2949	CA	GLN	390	17.064	26.722	7.352	1.00	39.30	1DIK3041
ATOM	2950	C	GLN	390	17.218	28.001	6.560	1.00	37.68	1DIK3042
ATOM	2951	O	GLN	390	16.399	28.306	5.687	1.00	38.67	1DIK3043
ATOM	2952	CB	GLN	390	17.336	25.488	6.493	1.00	42.00	1DIK3044
ATOM	2953	CG	GLN	390	18.614	24.779	6.890	1.00	53.74	1DIK3045
ATOM	2954	CD	GLN	390	18.668	23.361	6.364	1.00	63.83	1DIK3046
ATOM	2955	OE1	GLN	390	18.355	23.105	5.191	1.00	68.11	1DIK3047
ATOM	2956	NE2	GLN	390	19.065	22.421	7.224	1.00	63.91	1DIK3048
ATOM	2957	N	CYS	391	18.250	28.767	6.876	1.00	40.00	1DIK3049
ATOM	2958	CA	CYS	391	18.462	30.027	6.186	1.00	45.20	1DIK3050
ATOM	2959	C	CYS	391	19.823	30.061	5.521	1.00	49.70	1DIK3051
ATOM	2960	O	CYS	391	20.750	29.371	5.932	1.00	49.75	1DIK3052
ATOM	2961	CB	CYS	391	18.301	31.213	7.149	1.00	39.14	1DIK3053
ATOM	2962	SG	CYS	391	16.773	31.195	8.142	1.00	30.19	1DIK3054
ATOM	2963	N	GLN	392	19.917	30.883	4.488	1.00	59.92	1DIK3055
ATOM	2964	CA	GLN	392	21.121	31.044	3.685	1.00	68.58	1DIK3056
ATOM	2965	C	GLN	392	22.430	31.262	4.455	1.00	71.02	1DIK3057
ATOM	2966	O	GLN	392	23.442	30.618	4.166	1.00	72.41	1DIK3058
ATOM	2967	CB	GLN	392	20.883	32.199	2.724	1.00	73.43	1DIK3059
ATOM	2968	CG	GLN	392	21.760	32.223	1.498	1.00	80.79	1DIK3060
ATOM	2969	CD	GLN	392	21.489	33.465	0.686	1.00	83.73	1DIK3061

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ATOM	2983	CD	GLU	394	23.361	29.761	12.187	1.00	84.86	1DIK3075
ATOM	2984	OE1	GLU	394	23.242	30.948	12.578	1.00	86.06	1DIK3076
ATOM	2985	OE2	GLU	394	24.338	29.038	12.489	1.00	86.34	1DIK3077
ATOM	2986	N	GLN	395	24.077	27.608	9.314	1.00	67.62	1DIK3078
ATOM	2987	CA	GLN	395	24.296	26.203	8.924	1.00	67.27	1DIK3079
ATOM	2988	C	GLN	395	23.313	25.261	9.625	1.00	64.99	1DIK3080
ATOM	2989	O	GLN	395	22.818	24.294	9.034	1.00	65.93	1DIK3081
ATOM	2990	CB	GLN	395	25.704	25.752	9.288	1.00	70.58	1DIK3082
ATOM	2991	CG	GLN	395	26.799	26.627	8.760	1.00	80.49	1DIK3083
ATOM	2992	CD	GLN	395	28.085	26.437	9.542	1.00	86.58	1DIK3084
ATOM	2993	OE1	GLN	395	28.185	25.537	10.385	1.00	87.92	1DIK3085
ATOM	2994	NE2	GLN	395	29.077	27.280	9.272	1.00	90.05	1DIK3086
ATOM	2995	N	GLU	396	23.051	25.546	10.900	1.00	59.17	1DIK3087
ATOM	2996	CA	GLU	396	22.127	24.760	11.707	1.00	52.18	1DIK3088
ATOM	2997	C	GLU	396	20.694	25.250	11.536	1.00	45.17	1DIK3089
ATOM	2998	O	GLU	396	20.450	26.432	11.232	1.00	42.88	1DIK3090
ATOM	2999	CB	GLU	396	22.442	24.917	13.192	1.00	58.64	1DIK3091
ATOM	3000	CG	GLU	396	23.637	24.200	13.749	1.00	65.48	1DIK3092
ATOM	3001	CD	GLU	396	23.588	24.204	15.279	1.00	72.96	1DIK3093
ATOM	3002	OE1	GLU	396	22.721	23.485	15.849	1.00	75.18	1DIK3094
ATOM	3003	OE2	GLU	396	24.402	24.925	15.908	1.00	73.08	1DIK3095
ATOM	3004	N	PRO	397	19.723	24.344	11.708	1.00	37.24	1DIK3096
ATOM	3005	CA	PRO	397	18.346	24.817	11.572	1.00	33.03	1DIK3097
ATOM	3006	C	PRO	397	18.015	25.696	12.806	1.00	27.77	1DIK3098
ATOM	3007	O	PRO	397	18.547	25.491	13.912	1.00	23.86	1DIK3099
ATOM	3008	CB	PRO	397	17.537	23.515	11.499	1.00	30.60	1DIK3100
ATOM	3009	CG	PRO	397	18.343	22.572	12.325	1.00	34.10	1DIK3101
ATOM	3010	CD	PRO	397	19.779	22.897	11.975	1.00	33.21	1DIK3102
ATOM	3011	N	LEU	398	17.151	26.680	12.599	1.00	24.89	1DIK3103
ATOM	3012	CA	LEU	398	16.743	27.603	13.644	1.00	22.58	1DIK3104
ATOM	3013	C	LEU	398	15.287	27.333	14.072	1.00	23.54	1DIK3105
ATOM	3014	O	LEU	398	14.420	27.074	13.239	1.00	23.76	1DIK3106
ATCM	3015	CB	LEU	398	16.904	29.033	13.129	1.00	19.29	1DIK3107
ATOM	3016	CG	LEU	398	18.296	29.357	12.572	1.00	21.68	1DIK3108
ATOM	3017	CD1	LEU	398	18.210	30.505	11.590	1.00	21.80	1DIK3109
ATOM	3018	CD2	LEU	398	19.252	29.681	13.695	1.00	17.36	1DIK3110
ATOM	3019	N	VAL	399	15.039	27.395	15.374	1.00	23.51	1DIK3111
ATOM	3020	CA	VAL	399	13.727	27.149	15.959	1.00	23.57	1DIK3112
ATOM	3021	C	VAL	399	13.084	28.478	16.379	1.00	25.60	1DIK3113
ATOM	3022	O	VAL	399	13.767	29.398	16.832	1.00	28.79	1DIK3114
ATOM	3023	CB	VAL	399	13.864	26.226	17.220	1.00	23.92	1DIK3115
ATOM	3024	CG1	VAL	399	12.510	25.978	17.867	1.00	19.35	1DIK3116
ATOM	3025	CG2	VAL	399	14.525	24.906	16.844	1.00	19.06	1DIK3117
ATOM	3026	N	ARG	400	11.770	28.576	16.223	1.00	24.81	1DIK3118
ATOM	3027	CA	ARG	400	11.038	29.766	16.612	1.00	20.32	1DIK3119
ATOM	3028	C	ARG	400	9.642	29.348	17.060	1.00	20.66	1DIK3120
ATOM	3029	O	ARG	400	9.065	28.407	16.511	1.00	21.08	1DIK3121
ATOM	3030	CB	ARG	400	10.950	30.754	15.457	1.00	21.26	1DIK3122
ATOM	3031	CG	ARG	400	10.227	32.002	15.867	1.00	24.84	1DIK3123
ATOM	3032	CD	ARG	400	10.446	33.098	14.903	1.00	22.49	1DIK3124
ATOM	3033	NE	ARG	400	9.769	32.864	13.643	1.00	24.64	1DIK3125
ATOM	3034	CZ	ARG	400	9.536	33.835	12.763	1.00	33.02	1DIK3126
ATOM	3035	NH1	ARG	400	9.930	35.079	13.042	1.00	30.42	1DIK3127
ATOM	3036	NH2	ARG	400	8.915	33.576	11.614	1.00	30.09	1DIK3128
ATOM	3037	N	VAL	401	9.109	30.044	18.058	1.00	19.00	1DIK3129
ATOM	3038	CA	VAL	401	7.795	29.757	18.606	1.00	18.61	1DIK3130
ATOM	3039	C	VAL	401	6.882	30.980	18.554	1.00	21.25	1DIK3131
ATOM	3040	O	VAL	401	7.260	32.059	19.003	1.00	23.23	1DIK3132
ATOM	3041	CB	VAL	401	7.908	29.318	20.087	1.00	20.03	1DIK3133
ATOM	3042	CG1	VAL	401	6.529	29.173	20.701	1.00	17.45	1DIK3134
ATOM	3043	CG2	VAL	401	8.673	28.006	20.195	1.00	16.44	1DIK3135
ATOM	3044	N	LEU	402	5.683	30.812	18.006	1.00	20.98	1DIK3136
ATOM	3045	CA	LEU	402	4.701	31.888	17.948	1.00	17.41	1DIK3137
ATOM	3046	C	LEU	402	3.540	31.418	18.804	1.00	19.37	1DIK3138
ATOM	3047	O	LEU	402	3.165	30.249	18.728	1.00	22.64	1DIK3139
ATOM	3048	CB	LEU	402	4.206	32.128	16.519	1.00	14.63	1DIK3140
ATOM	3049	CG	LEU	402	5.213	32.709	15.523	1.00	17.85	1DIK3141
ATOM	3050	CD1	LEU	402	6.046	31.608	14.893	1.00	12.36	1DIK3142
ATOM	3051	CD2	LEU	402	4.464	33.480	14.461	1.00	15.05	1DIK3143
ATOM	3052	N	VAL	403	2.984	32.305	19.626	1.00	18.51	1DIK3144
ATOM	3053	CA	VAL	403	1.831	31.962	20.472	1.00	18.78	1DIK3145
ATOM	3054	C	VAL	403	0.710	32.925	20.081</td			

Figure 8/38

ATOM	3068	CA	ASP	405	0.657	35.003	16.317	1.00	21.55	1DIK3160
ATOM	3069	C	ASP	405	1.704	35.960	16.838	1.00	24.70	1DIK3161
ATOM	3070	O	ASP	405	2.244	36.765	16.078	1.00	27.69	1DIK3162
ATOM	3071	CB	ASP	405	-0.374	35.753	15.481	1.00	19.33	1DIK3163
ATOM	3072	CG	ASP	405	-1.249	34.821	14.694	1.00	21.06	1DIK3164
ATOM	3073	OD1	ASP	405	-0.824	33.668	14.469	1.00	22.07	1DIK3165
ATOM	3074	OD2	ASP	405	-2.359	35.231	14.303	1.00	23.53	1DIK3166
ATOM	3075	N	ARG	406	1.999	35.874	18.126	1.00	24.97	1DIK3167
ATOM	3076	CA	ARG	406	3.022	36.732	18.709	1.00	25.69	1DIK3168
ATOM	3077	C	ARG	406	4.317	35.917	18.738	1.00	24.24	1DIK3169
ATOM	3078	O	ARG	406	4.313	34.767	19.213	1.00	24.35	1DIK3170
ATOM	3079	CB	ARG	406	2.619	37.141	20.139	1.00	26.35	1DIK3171
ATOM	3080	CG	ARG	406	3.618	38.049	20.840	1.00	26.41	1DIK3172
ATOM	3081	CD	ARG	406	3.315	38.224	22.331	1.00	28.94	1DIK3173
ATOM	3082	NE	ARG	406	4.501	38.715	23.031	1.00	32.36	1DIK3174
ATOM	3083	CZ	ARG	406	5.099	38.092	24.047	1.00	36.19	1DIK3175
ATOM	3084	NH1	ARG	406	4.613	36.950	24.521	1.00	35.65	1DIK3176
ATOM	3085	NH2	ARG	406	6.188	38.618	24.601	1.00	38.62	1DIK3177
ATOM	3086	N	VAL	407	5.410	36.483	18.226	1.00	20.04	1DIK3178
ATOM	3087	CA	VAL	407	6.689	35.779	18.266	1.00	19.32	1DIK3179
ATOM	3088	C	VAL	407	7.183	35.895	19.710	1.00	22.20	1DIK3180
ATOM	3089	O	VAL	407	7.481	36.974	20.198	1.00	26.19	1DIK3181
ATOM	3090	CB	VAL	407	7.743	36.372	17.276	1.00	17.66	1DIK3182
ATOM	3091	CG1	VAL	407	9.143	35.815	17.606	1.00	12.58	1DIK3183
ATOM	3092	CG2	VAL	407	7.367	36.031	15.826	1.00	8.62	1DIK3184
ATOM	3093	N	VAL	408	7.245	34.767	20.391	1.00	27.04	1DIK3185
ATOM	3094	CA	VAL	408	7.682	34.718	21.779	1.00	30.49	1DIK3186
ATOM	3095	C	VAL	408	9.169	34.371	21.845	1.00	33.80	1DIK3187
ATOM	3096	O	VAL	408	9.576	33.273	21.468	1.00	36.38	1DIK3188
ATOM	3097	CB	VAL	408	6.869	33.645	22.575	1.00	27.31	1DIK3189
ATOM	3098	CG1	VAL	408	7.310	33.590	24.026	1.00	26.14	1DIK3190
ATOM	3099	CG2	VAL	408	5.392	33.950	22.493	1.00	25.33	1DIK3191
ATOM	3100	N	PRO	409	10.007	35.312	22.298	1.00	39.45	1DIK3192
ATOM	3101	CA	PRO	409	11.453	35.048	22.405	1.00	39.88	1DIK3193
ATOM	3102	C	PRO	409	11.740	33.855	23.348	1.00	38.92	1DIK3194
ATOM	3103	O	PRO	409	11.135	33.707	24.423	1.00	36.45	1DIK3195
ATOM	3104	CB	PRO	409	12.005	36.368	22.948	1.00	42.97	1DIK3196
ATOM	3105	CG	PRO	409	10.992	37.396	22.418	1.00	44.48	1DIK3197
ATOM	3106	CD	PRO	409	9.688	36.692	22.702	1.00	40.36	1DIK3198
ATOM	3107	N	LEU	410	12.668	33.009	22.921	1.00	38.46	1DIK3199
ATOM	3108	CA	LEU	410	13.041	31.814	23.660	1.00	34.48	1DIK3200
ATOM	3109	C	LEU	410	13.959	32.117	24.846	1.00	33.51	1DIK3201
ATOM	3110	O	LEU	410	14.710	33.092	24.839	1.00	31.11	1DIK3202
ATOM	3111	CB	LEU	410	13.707	30.810	22.697	1.00	32.83	1DIK3203
ATOM	3112	CG	LEU	410	12.875	30.372	21.476	1.00	29.37	1DIK3204
ATOM	3113	CD1	LEU	410	13.725	29.543	20.528	1.00	28.62	1DIK3205
ATOM	3114	CD2	LEU	410	11.661	29.584	21.937	1.00	24.58	1DIK3206
ATOM	3115	N	HIS	411	13.888	31.275	25.867	1.00	32.47	1DIK3207
ATOM	3116	CA	HIS	411	14.725	31.432	27.041	1.00	34.54	1DIK3208
ATOM	3117	C	HIS	411	15.585	30.188	27.209	1.00	33.85	1DIK3209
ATOM	3118	O	HIS	411	15.168	29.088	26.854	1.00	36.81	1DIK3210
ATOM	3119	CB	HIS	411	13.865	31.652	28.288	1.00	40.62	1DIK3211
ATOM	3120	CG	HIS	411	13.249	33.012	28.352	1.00	43.65	1DIK3212
ATOM	3121	ND1	HIS	411	11.994	33.287	27.854	1.00	46.21	1DIK3213
ATOM	3122	CD2	HIS	411	13.731	34.185	28.822	1.00	43.54	1DIK3214
ATOM	3123	CE1	HIS	411	11.731	34.571	28.012	1.00	46.39	1DIK3215
ATOM	3124	NE2	HIS	411	12.771	35.138	28.598	1.00	43.29	1DIK3216
ATOM	3125	N	GLY	412	16.786	30.372	27.747	1.00	32.45	1DIK3217
ATOM	3126	CA	GLY	412	17.690	29.258	27.961	1.00	27.18	1DIK3218
ATOM	3127	C	GLY	412	18.642	29.036	26.807	1.00	28.45	1DIK3219
ATOM	3128	O	GLY	412	19.530	28.180	26.880	1.00	32.18	1DIK3220
ATOM	3129	N	CYS	413	18.470	29.797	25.734	1.00	25.33	1DIK3221
ATOM	3130	CA	CYS	413	19.334	29.669	24.570	1.00	24.44	1DIK3222
ATOM	3131	C	CYS	413	19.542	31.073	24.032	1.00	23.08	1DIK3223
ATOM	3132	O	CYS	413	18.723	31.967	24.278	1.00	23.15	1DIK3224
ATOM	3133	CB	CYS	413	18.691	28.751	23.511	1.00	26.97	1DIK3225
ATOM	3134	SG	CYS	413	17.010	29.217	22.959	1.00	26.06	1DIK3226
ATOM	3135	N	PRO	414	20.640	31.289	23.299	1.00	22.53	1DIK3227
ATOM	3136	CA	PRO	414	21.000	32.586	22.706	1.00	25.51	1DIK3228
ATOM	3137	C	PRO	414	20.086	32.989	21.542	1.00	26.43	1DIK3229
ATOM	3138	O	PRO	414	20.303	32.531	20.415	1.00	24.37	1DIK3230
ATOM	3139	CB	PRO	414	22.438	32.359	22.202	1.00	27.32	1DIK3231

Figure 8/39

ATOM	3153	CB	ASP	416	19.265	35.579	16.207	1.00	22.64	1DIK3245
ATOM	3154	CG	ASP	416	18.085	34.947	15.445	1.00	25.90	1DIK3246
ATOM	3155	OD1	ASP	416	16.896	35.237	15.713	1.00	28.90	1DIK3247
ATOM	3156	OD2	ASP	416	18.366	34.135	14.540	1.00	24.59	1DIK3248
ATOM	3157	N	ALA	417	18.062	38.327	16.619	1.00	25.89	1DIK3249
ATOM	3158	CA	ALA	417	17.137	39.443	16.411	1.00	26.04	1DIK3250
ATOM	3159	C	ALA	417	15.717	39.053	15.986	1.00	27.35	1DIK3251
ATOM	3160	O	ALA	417	14.779	39.837	16.165	1.00	28.16	1DIK3252
ATOM	3161	CB	ALA	417	17.738	40.443	15.403	1.00	22.45	1DIK3253
ATOM	3162	N	LEU	418	15.553	37.852	15.428	1.00	28.60	1DIK3254
ATOM	3163	CA	LEU	418	14.238	37.384	14.991	1.00	26.36	1DIK3255
ATOM	3164	C	LEU	418	13.552	36.391	15.952	1.00	26.54	1DIK3256
ATOM	3165	O	LEU	418	12.533	35.795	15.608	1.00	26.72	1DIK3257
ATOM	3166	CB	LEU	418	14.329	36.829	13.564	1.00	25.45	1DIK3258
ATOM	3167	CG	LEU	418	14.649	37.875	12.474	1.00	28.70	1DIK3259
ATOM	3168	CD1	LEU	418	14.842	37.187	11.139	1.00	27.85	1DIK3260
ATOM	3169	CD2	LEU	418	13.525	38.908	12.354	1.00	23.85	1DIK3261
ATOM	3170	N	GLY	419	14.118	36.234	17.154	1.00	27.13	1DIK3262
ATOM	3171	CA	GLY	419	13.556	35.364	18.182	1.00	22.28	1DIK3263
ATOM	3172	C	GLY	419	13.913	33.894	18.094	1.00	25.13	1DIK3264
ATOM	3173	O	GLY	419	13.347	33.077	18.827	1.00	29.64	1DIK3265
ATOM	3174	N	ARG	420	14.852	33.555	17.218	1.00	18.88	1DIK3266
ATOM	3175	CA	ARG	420	15.252	32.173	17.004	1.00	21.64	1DIK3267
ATOM	3176	C	ARG	420	16.483	31.695	17.768	1.00	23.83	1DIK3268
ATOM	3177	O	ARG	420	17.306	32.495	18.193	1.00	26.72	1DIK3269
ATOM	3178	CB	ARG	420	15.504	31.959	15.515	1.00	23.45	1DIK3270
ATOM	3179	CG	ARG	420	14.413	32.532	14.623	1.00	27.05	1DIK3271
ATOM	3180	CD	ARG	420	14.827	32.520	13.166	1.00	25.37	1DIK3272
ATOM	3181	NE	ARG	420	16.019	33.333	12.915	1.00	30.86	1DIK3273
ATOM	3182	CZ	ARG	420	16.435	33.730	11.708	1.00	28.82	1DIK3274
ATOM	3183	NH1	ARG	420	15.775	33.407	10.599	1.00	25.15	1DIK3275
ATOM	3184	NH2	ARG	420	17.528	34.463	11.608	1.00	28.95	1DIK3276
ATOM	3185	N	CYS	421	16.590	30.377	17.927	1.00	24.78	1DIK3277
ATOM	3186	CA	CYS	421	17.726	29.704	18.570	1.00	22.57	1DIK3278
ATOM	3187	C	CYS	421	18.039	28.519	17.679	1.00	23.03	1DIK3279
ATOM	3188	O	CYS	421	17.144	27.988	17.035	1.00	22.43	1DIK3280
ATOM	3189	CB	CYS	421	17.366	29.144	19.944	1.00	22.26	1DIK3281
ATOM	3190	SG	CYS	421	17.337	30.349	21.302	1.00	27.11	1DIK3282
ATOM	3191	N	THR	422	19.294	28.098	17.623	1.00	26.80	1DIK3283
ATOM	3192	CA	THR	422	19.624	26.935	16.816	1.00	26.97	1DIK3284
ATOM	3193	C	THR	422	18.879	25.795	17.511	1.00	30.20	1DIK3285
ATOM	3194	O	THR	422	18.636	25.857	18.731	1.00	30.05	1DIK3286
ATOM	3195	CB	THR	422	21.146	26.649	16.799	1.00	25.67	1DIK3287
ATOM	3196	OG1	THR	422	21.615	26.400	18.133	1.00	25.43	1DIK3288
ATOM	3197	CG2	THR	422	21.895	27.827	16.200	1.00	23.71	1DIK3289
ATOM	3198	N	ARG	423	18.505	24.767	16.752	1.00	30.48	1DIK3290
ATOM	3199	CA	ARG	423	17.781	23.650	17.331	1.00	28.62	1DIK3291
ATOM	3200	C	ARG	423	18.528	23.048	18.518	1.00	29.61	1DIK3292
ATOM	3201	O	ARG	423	17.934	22.791	19.567	1.00	29.29	1DIK3293
ATOM	3202	CB	ARG	423	17.536	22.573	16.281	1.00	27.71	1DIK3294
ATOM	3203	CG	ARG	423	16.711	21.420	16.820	1.00	30.71	1DIK3295
ATOM	3204	CD	ARG	423	16.689	20.273	15.857	1.00	31.47	1DIK3296
ATOM	3205	NE	ARG	423	18.046	19.852	15.553	1.00	33.67	1DIK3297
ATOM	3206	CZ	ARG	423	18.406	19.262	14.422	1.00	31.99	1DIK3298
ATOM	3207	NH1	ARG	423	17.510	19.012	13.476	1.00	35.49	1DIK3299
ATOM	3208	NH2	ARG	423	19.671	18.921	14.241	1.00	38.78	1DIK3300
ATOM	3209	N	ASP	424	19.830	22.838	18.351	1.00	29.32	1DIK3301
ATOM	3210	CA	ASP	424	20.654	22.238	19.393	1.00	32.19	1DIK3302
ATOM	3211	C	ASP	424	20.729	22.998	20.704	1.00	30.97	1DIK3303
ATOM	3212	O	ASP	424	20.614	22.391	21.772	1.00	35.15	1DIK3304
ATOM	3213	CB	ASP	424	22.057	21.954	18.858	1.00	37.79	1DIK3305
ATOM	3214	CG	ASP	424	22.087	20.758	17.900	1.00	49.74	1DIK3306
ATOM	3215	OD1	ASP	424	21.108	20.531	17.136	1.00	52.55	1DIK3307
ATOM	3216	OD2	ASP	424	23.101	20.034	17.911	1.00	52.75	1DIK3308
ATOM	3217	N	SER	425	20.919	24.311	20.653	1.00	28.34	1DIK3309
ATOM	3218	CA	SER	425	20.976	25.071	21.893	1.00	28.79	1DIK3310
ATOM	3219	C	SER	425	19.568	25.148	22.304	1.00	28.14	1DIK3311
ATOM	3220	O	SER	425	19.422	25.177	23.731	1.00	27.74	1DIK3312
ATOM	3221	CB	SER	425	21.584	26.470	21.674	1.00	27.42	1DIK3313
ATOM	3222	OG	SER	425	20.849	27.235	20.742	1.00	31.04	1DIK3314
ATOM	3223	N	PHE	426	18.538	25.170	21.651	1.00	26.40	1DIK3315
ATOM	3224	CA	PHE	426	17.152	25.203	22.129</td			

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ATOM	3238	CB	VAL	427	17.348	20.346	22.047	1.00	28.39	1DIK3330
ATOM	3239	CG1	VAL	427	17.439	19.022	22.809	1.00	26.94	1DIK3331
ATOM	3240	CG2	VAL	427	16.326	20.256	20.901	1.00	24.93	1DIK3332
ATOM	3241	N	ARG	428	19.024	21.909	24.160	1.00	31.56	1DIK3333
ATOM	3242	CA	ARG	428	19.931	21.947	25.292	1.00	33.59	1DIK3334
ATOM	3243	C	ARG	428	19.331	22.797	26.426	1.00	32.27	1DIK3335
ATOM	3244	O	ARG	428	19.489	22.472	27.598	1.00	31.56	1DIK3336
ATOM	3245	CB	ARG	428	21.257	22.518	24.819	1.00	40.23	1DIK3337
ATOM	3246	CG	ARG	428	22.404	22.306	25.750	1.00	55.44	1DIK3338
ATOM	3247	CD	ARG	428	23.706	22.643	25.043	1.00	69.03	1DIK3339
ATOM	3248	NE	ARG	428	24.726	23.025	26.013	1.00	83.02	1DIK3340
ATOM	3249	CZ	ARG	428	25.632	23.981	25.819	1.00	88.04	1DIK3341
ATOM	3250	NH1	ARG	428	25.659	24.656	24.674	1.00	89.88	1DIK3342
ATOM	3251	NH2	ARG	428	26.516	24.260	26.777	1.00	89.48	1DIK3343
ATOM	3252	N	GLY	429	18.634	23.875	26.068	1.00	31.73	1DIK3344
ATOM	3253	CA	GLY	429	18.011	24.754	27.049	1.00	29.88	1DIK3345
ATOM	3254	C	GLY	429	16.814	24.187	27.816	1.00	31.65	1DIK3346
ATOM	3255	O	GLY	429	16.434	24.718	28.871	1.00	29.27	1DIK3347
ATOM	3256	N	LEU	430	16.208	23.115	27.308	1.00	32.28	1DIK3348
ATOM	3257	CA	LEU	430	15.057	22.495	27.977	1.00	31.40	1DIK3349
ATOM	3258	C	LEU	430	15.546	21.456	29.009	1.00	30.50	1DIK3350
ATOM	3259	O	LEU	430	15.093	20.307	29.033	1.00	30.10	1DIK3351
ATOM	3260	CB	LEU	430	14.144	21.836	26.930	1.00	27.85	1DIK3352
ATOM	3261	CG	LEU	430	13.635	22.755	25.819	1.00	27.51	1DIK3353
ATOM	3262	CD1	LEU	430	12.980	21.956	24.702	1.00	21.48	1DIK3354
ATOM	3263	CD2	LEU	430	12.672	23.751	26.420	1.00	21.75	1DIK3355
ATOM	3264	N	SER	431	16.468	21.869	29.869	1.00	29.03	1DIK3356
ATOM	3265	CA	SER	431	17.028	20.960	30.864	1.00	31.21	1DIK3357
ATOM	3266	C	SER	431	15.991	20.465	31.871	1.00	28.76	1DIK3358
ATOM	3267	O	SER	431	16.037	19.308	32.290	1.00	29.64	1DIK3359
ATOM	3268	CB	SER	431	18.212	21.623	31.580	1.00	31.70	1DIK3360
ATOM	3269	OG	SER	431	17.837	22.857	32.169	1.00	36.73	1DIK3361
ATOM	3270	N	PHE	432	15.059	21.334	32.254	1.00	25.33	1DIK3362
ATOM	3271	CA	PHE	432	14.016	20.969	33.207	1.00	26.36	1DIK3363
ATOM	3272	C	PHE	432	13.170	19.796	32.681	1.00	30.38	1DIK3364
ATOM	3273	O	PHE	432	12.904	18.822	33.404	1.00	29.32	1DIK3365
ATOM	3274	CB	PHE	432	13.133	22.186	33.487	1.00	21.52	1DIK3366
ATOM	3275	CG	PHE	432	11.908	21.885	34.315	1.00	24.46	1DIK3367
ATOM	3276	CD1	PHE	432	12.022	21.567	35.670	1.00	22.91	1DIK3368
ATOM	3277	CD2	PHE	432	10.636	21.941	33.739	1.00	19.38	1DIK3369
ATOM	3278	CE1	PHE	432	10.883	21.311	36.441	1.00	24.30	1DIK3370
ATOM	3279	CE2	PHE	432	9.489	21.688	34.495	1.00	22.66	1DIK3371
ATOM	3280	CZ	PHE	432	9.606	21.372	35.846	1.00	26.15	1DIK3372
ATOM	3281	N	ALA	433	12.752	19.896	31.421	1.00	27.75	1DIK3373
ATOM	3282	CA	ALA	433	11.958	18.850	30.796	1.00	26.55	1DIK3374
ATOM	3283	C	ALA	433	12.789	17.577	30.597	1.00	25.17	1DIK3375
ATOM	3284	O	ALA	433	12.350	16.492	30.974	1.00	28.47	1DIK3376
ATOM	3285	CB	ALA	433	11.411	19.336	29.460	1.00	23.17	1DIK3377
ATOM	3286	N	ARG	434	13.982	17.710	30.018	1.00	23.09	1DIK3378
ATOM	3287	CA	ARG	434	14.849	16.557	29.754	1.00	24.40	1DIK3379
ATOM	3288	C	ARG	434	15.156	15.725	30.992	1.00	24.98	1DIK3380
ATOM	3289	O	ARG	434	15.416	14.525	30.889	1.00	25.10	1DIK3381
ATOM	3290	CB	ARG	434	16.163	16.991	29.087	1.00	22.29	1DIK3382
ATOM	3291	CG	ARG	434	16.013	17.379	27.610	1.00	27.82	1DIK3383
ATOM	3292	CD	ARG	434	17.363	17.590	26.910	1.00	29.10	1DIK3384
ATOM	3293	NE	ARG	434	18.090	18.741	27.446	1.00	36.82	1DIK3385
ATOM	3294	CZ	ARG	434	19.087	18.664	28.332	1.00	39.13	1DIK3386
ATOM	3295	NH1	ARG	434	19.487	17.480	28.784	1.00	39.16	1DIK3387
ATOM	3296	NH2	ARG	434	19.688	19.770	28.766	1.00	30.93	1DIK3388
ATOM	3297	N	SER	435	15.123	16.367	32.157	1.00	26.13	1DIK3389
ATOM	3298	CA	SER	435	15.394	15.696	33.427	1.00	28.09	1DIK3390
ATOM	3299	C	SER	435	14.126	15.122	34.088	1.00	26.80	1DIK3391
ATOM	3300	O	SER	435	14.208	14.433	35.103	1.00	27.78	1DIK3392
ATOM	3301	CB	SER	435	16.112	16.659	34.392	1.00	29.48	1DIK3393
ATOM	3302	OG	SER	435	15.322	17.811	34.687	1.00	36.42	1DIK3394
ATOM	3303	N	GLY	436	12.960	15.407	33.515	1.00	26.30	1DIK3395
ATOM	3304	CA	GLY	436	11.719	14.894	34.068	1.00	24.08	1DIK3396
ATOM	3305	C	GLY	436	11.003	15.827	35.025	1.00	25.00	1DIK3397
ATOM	3306	O	GLY	436	10.114	15.383	35.763	1.00	25.04	1DIK3398
ATOM	3307	N	GLY	437	11.376	17.107	35.015	1.00	24.66	1DIK3399
ATOM	3308	CA	GLY	437	10.755	18.076	35.901	1.00	26.30	1DIK3400
ATOM	3309	C	GLY	437	10.743	17.560	37.330			

Figure 8/41

ATOM	3323	CB	TRP	439	7.545	13.573	37.045	1.00	23.82	1DIK3415
ATOM	3324	CG	TRP	439	6.379	12.641	36.794	1.00	25.59	1DIK3416
ATOM	3325	CD1	TRP	439	6.331	11.304	37.067	1.00	22.86	1DIK3417
ATOM	3326	CD2	TRP	439	5.076	12.989	36.279	1.00	25.24	1DIK3418
ATOM	3327	NE1	TRP	439	5.089	10.802	36.764	1.00	27.19	1DIK3419
ATOM	3328	CE2	TRP	439	4.299	11.813	36.280	1.00	25.01	1DIK3420
ATOM	3329	CE3	TRP	439	4.494	14.179	35.819	1.00	25.14	1DIK3421
ATOM	3330	CZ2	TRP	439	2.967	11.790	35.842	1.00	26.41	1DIK3422
ATOM	3331	CZ3	TRP	439	3.169	14.157	35.381	1.00	21.25	1DIK3423
ATOM	3332	CH2	TRP	439	2.424	12.970	35.398	1.00	27.53	1DIK3424
ATOM	3333	N	ALA	440	8.608	13.198	40.147	1.00	39.08	1DIK3425
ATOM	3334	CA	ALA	440	8.740	12.325	41.304	1.00	40.38	1DIK3426
ATOM	3335	C	ALA	440	7.703	12.771	42.429	1.00	42.18	1DIK3427
ATOM	3336	O	ALA	440	7.072	11.948	43.026	1.00	44.41	1DIK3428
ATOM	3337	CB	ALA	440	10.173	12.341	41.776	1.00	36.80	1DIK3429
ATOM	3338	N	GLU	441	7.758	14.077	42.689	1.00	41.96	1DIK3430
ATOM	3339	CA	GLU	441	6.903	14.687	43.713	1.00	42.69	1DIK3431
ATOM	3340	C	GLU	441	5.397	14.402	43.529	1.00	42.04	1DIK3432
ATOM	3341	O	GLU	441	4.575	14.766	44.373	1.00	42.51	1DIK3433
ATOM	3342	CB	GLU	441	7.109	16.207	43.710	1.00	49.22	1DIK3434
ATOM	3343	CG	GLU	441	8.554	16.671	43.787	1.00	56.93	1DIK3435
ATOM	3344	CD	GLU	441	9.184	16.346	45.122	1.00	65.76	1DIK3436
ATOM	3345	OE1	GLU	441	8.602	16.733	46.161	1.00	69.69	1DIK3437
ATOM	3346	OE2	GLU	441	10.260	15.704	45.139	1.00	69.76	1DIK3438
ATOM	3347	N	CYS	442	5.034	13.765	42.426	1.00	39.99	1DIK3439
ATOM	3348	CA	CYS	442	3.638	13.468	42.160	1.00	40.48	1DIK3440
ATOM	3349	C	CYS	442	3.068	12.411	43.073	1.00	43.32	1DIK3441
ATOM	3350	O	CYS	442	1.859	12.405	43.337	1.00	43.60	1DIK3442
ATOM	3351	CB	CYS	442	3.452	12.982	40.715	1.00	39.39	1DIK3443
ATOM	3352	SG	CYS	442	3.541	14.265	39.429	1.00	32.94	1DIK3444
ATOM	3353	N	PHE	443	3.930	11.517	43.546	1.00	45.06	1DIK3445
ATOM	3354	CA	PHE	443	3.479	10.403	44.372	1.00	50.79	1DIK3446
ATOM	3355	C	PHE	443	3.941	10.416	45.813	1.00	55.76	1DIK3447
ATOM	3356	O	PHE	443	3.268	9.863	46.684	1.00	57.52	1DIK3448
ATOM	3357	CB	PHE	443	3.882	9.111	43.681	1.00	45.54	1DIK3449
ATOM	3358	CG	PHE	443	3.724	9.182	42.205	1.00	45.83	1DIK3450
ATOM	3359	CD1	PHE	443	2.453	9.192	41.636	1.00	43.41	1DIK3451
ATOM	3360	CD2	PHE	443	4.840	9.294	41.379	1.00	46.74	1DIK3452
ATOM	3361	CE1	PHE	443	2.292	9.315	40.262	1.00	43.31	1DIK3453
ATOM	3362	CE2	PHE	443	4.694	9.417	39.999	1.00	45.78	1DIK3454
ATOM	3363	CZ	PHE	443	3.416	9.428	39.441	1.00	45.42	1DIK3455
ATOM	3364	N	ALA	444	5.089	11.039	46.060	1.00	62.20	1DIK3456
ATOM	3365	CA	ALA	444	5.621	11.144	47.412	1.00	66.60	1DIK3457
ATOM	3366	C	ALA	444	4.893	12.333	48.043	1.00	68.05	1DIK3458
ATOM	3367	O	ALA	444	3.938	12.089	48.817	1.00	68.94	1DIK3459
ATOM	3368	CB	ALA	444	7.151	11.380	47.381	1.00	66.83	1DIK3460
ATOM	3369	OXT	ALA	444	5.274	13.489	47.747	1.00	69.24	1DIK3461
TER	3370	ALA		444						1DIK3462
HETATM	3371	O	HOH	1	5.314	11.951	16.327	1.00	10.28	1DIK3463
HETATM	3372	O	HOH	2	-6.660	26.826	16.721	1.00	14.37	1DIK3464
HETATM	3373	O	HOH	3	0.327	31.364	16.394	1.00	14.78	1DIK3465
HETATM	3374	O	HOH	4	-11.448	9.894	26.651	1.00	15.14	1DIK3466
HETATM	3375	O	HOH	5	-1.808	14.907	36.587	1.00	15.18	1DIK3467
HETATM	3376	O	HOH	6	-16.607	13.889	26.028	1.00	15.50	1DIK3468
HETATM	3377	O	HOH	7	8.014	7.031	26.624	1.00	15.90	1DIK3469
HETATM	3378	O	HOH	8	2.890	16.506	29.187	1.00	16.33	1DIK3470
HETATM	3379	O	HOH	9	-3.509	12.674	9.344	1.00	16.84	1DIK3471
HETATM	3380	O	HOH	10	12.661	12.918	24.069	1.00	17.03	1DIK3472
HETATM	3381	O	HOH	11	0.759	15.125	16.187	1.00	18.48	1DIK3473
HETATM	3382	O	HOH	12	-4.619	39.381	32.613	1.00	18.74	1DIK3474
HETATM	3383	O	HOH	13	-9.462	31.056	14.118	1.00	18.80	1DIK3475
HETATM	3384	O	HOH	14	-5.677	35.681	21.397	1.00	19.53	1DIK3476
HETATM	3385	O	HOH	15	-11.372	5.811	26.977	1.00	20.29	1DIK3477
HETATM	3386	O	HOH	16	1.644	9.234	20.239	1.00	20.38	1DIK3478
HETATM	3387	O	HOH	17	7.980	5.282	24.219	1.00	20.45	1DIK3479
HETATM	3388	O	HOH	18	-2.840	6.618	26.553	1.00	21.48	1DIK3480
HETATM	3389	O	HOH	19	10.194	6.545	20.888	1.00	21.50	1DIK3481
HETATM	3390	O	HOH	20	-10.932	8.587	24.215	1.00	22.02	1DIK3482
HETATM	3391	O	HOH	21	-3.698	27.479	12.828	1.00	22.24	1DIK3483
HETATM	3392	O	HOH	22	-9.209	6.732	23.045	1.00	22.35	1DIK3484
HETATM	3393	O	HOH	23	-11.843	33.526	16.995	1.00	22.95	1DIK3485
HETATM	3394	O	HOH	24	-10.730	33.322	13.268	1.00	23.32	1DIK3486
HETATM	3395	O	HOH	25	-5.					

Figure 8/42

HETATM	3408	O	HOH	38	-12.921	16.340	9.063	1.00	27.46	1DIK3500
HETATM	3409	O	HOH	39	-12.574	24.639	28.242	1.00	27.73	1DIK3501
HETATM	3410	O	HOH	40	-12.507	26.784	33.545	1.00	27.75	1DIK3502
HETATM	3411	O	HOH	41	-7.187	31.641	12.393	1.00	27.85	1DIK3503
HETATM	3412	O	HOH	42	10.571	32.202	19.033	1.00	28.02	1DIK3504
HETATM	3413	O	HOH	43	8.426	35.536	30.142	1.00	28.34	1DIK3505
HETATM	3414	O	HOH	44	-6.691	36.766	30.786	1.00	28.87	1DIK3506
HETATM	3415	O	HOH	45	12.389	22.580	30.279	1.00	29.03	1DIK3507
HETATM	3416	O	HOH	46	-16.222	15.844	27.511	1.00	29.03	1DIK3508
HETATM	3417	O	HOH	47	-10.420	13.136	6.619	1.00	29.13	1DIK3509
HETATM	3418	O	HOH	48	6.987	21.974	38.216	1.00	29.26	1DIK3510
HETATM	3419	O	HOH	49	-17.438	17.382	24.990	1.00	29.33	1DIK3511
HETATM	3420	O	HOH	50	-22.489	30.175	17.758	1.00	29.51	1DIK3512
HETATM	3421	O	HOH	51	-2.152	40.434	32.506	1.00	29.67	1DIK3513
HETATM	3422	O	HOH	52	-10.794	11.992	11.258	1.00	29.84	1DIK3514
HETATM	3423	O	HOH	53	-5.062	39.959	28.886	1.00	29.89	1DIK3515
HETATM	3424	O	HOH	54	-19.008	30.051	23.934	1.00	29.97	1DIK3516
HETATM	3425	O	HOH	55	14.324	12.475	22.179	1.00	29.97	1DIK3517
HETATM	3426	O	HOH	56	-15.744	47.285	28.530	1.00	29.97	1DIK3518
HETATM	3427	O	HOH	57	-2.017	21.298	33.876	1.00	30.51	1DIK3519
HETATM	3428	O	HOH	58	-10.164	23.699	27.468	1.00	30.66	1DIK3520
HETATM	3429	O	HOH	59	21.068	30.466	19.064	1.00	30.86	1DIK3521
HETATM	3430	O	HOH	60	15.633	26.247	25.288	1.00	31.46	1DIK3522
HETATM	3431	O	HOH	61	2.539	13.006	3.675	1.00	31.51	1DIK3523
HETATM	3432	O	HOH	62	0.718	11.503	8.049	1.00	31.69	1DIK3524
HETATM	3433	O	HOH	63	6.296	32.820	36.174	1.00	31.69	1DIK3525
HETATM	3434	O	HOH	64	-6.588	42.450	32.884	1.00	31.91	1DIK3526
HETATM	3435	O	HOH	65	2.321	35.791	25.121	1.00	32.04	1DIK3527
HETATM	3436	O	HOH	66	-11.516	36.087	6.335	1.00	32.59	1DIK3528
HETATM	3437	O	HOH	67	-25.724	25.284	29.618	1.00	32.59	1DIK3529
HETATM	3438	O	HOH	68	-18.133	26.391	31.970	1.00	32.62	1DIK3530
HETATM	3439	O	HOH	69	-14.947	45.064	46.354	1.00	33.42	1DIK3531
HETATM	3440	O	HOH	70	21.082	26.576	25.533	1.00	33.44	1DIK3532
HETATM	3441	O	HOH	71	11.263	14.005	39.063	1.00	33.76	1DIK3533
HETATM	3442	O	HOH	72	6.695	36.561	26.464	1.00	33.92	1DIK3534
HETATM	3443	O	HOH	73	-5.225	27.878	-1.684	1.00	34.01	1DIK3535
HETATM	3444	O	HOH	74	-0.802	9.860	-0.093	1.00	34.16	1DIK3536
HETATM	3445	O	HOH	75	-12.291	22.260	29.152	1.00	34.19	1DIK3537
HETATM	3446	O	HOH	76	9.096	28.265	3.852	1.00	35.19	1DIK3538
HETATM	3447	O	HOH	77	14.838	41.703	18.071	1.00	35.41	1DIK3539
HETATM	3448	O	HOH	78	7.786	14.132	5.764	1.00	35.54	1DIK3540
HETATM	3449	O	HOH	79	14.772	24.028	31.196	1.00	35.79	1DIK3541
HETATM	3450	O	HOH	80	-6.978	43.656	22.677	1.00	35.90	1DIK3542
HETATM	3451	O	HOH	81	-10.032	8.600	15.243	1.00	36.00	1DIK3543
HETATM	3452	O	HOH	82	24.248	25.836	18.908	1.00	36.04	1DIK3544
HETATM	3453	O	HOH	83	-9.437	28.721	1.634	1.00	36.20	1DIK3545
HETATM	3454	O	HOH	84	-2.779	26.774	21.988	1.00	36.25	1DIK3546
HETATM	3455	O	HOH	85	-20.467	37.474	17.552	1.00	36.27	1DIK3547
HETATM	3456	O	HOH	86	8.166	29.232	31.117	1.00	36.46	1DIK3548
HETATM	3457	O	HOH	87	-26.538	28.576	41.161	1.00	36.47	1DIK3549
HETATM	3458	O	HOH	88	-2.580	22.992	47.692	1.00	36.48	1DIK3550
HETATM	3459	O	HOH	89	12.366	14.284	9.003	1.00	36.58	1DIK3551
HETATM	3460	O	HOH	90	-21.790	30.576	46.190	1.00	36.67	1DIK3552
HETATM	3461	O	HOH	91	-15.282	25.935	33.446	1.00	36.75	1DIK3553
HETATM	3462	O	HOH	92	14.144	14.560	25.959	1.00	36.89	1DIK3554
HETATM	3463	O	HOH	93	-1.689	11.245	32.455	1.00	36.99	1DIK3555
HETATM	3464	O	HOH	94	-15.117	10.158	15.158	1.00	37.08	1DIK3556
HETATM	3465	O	HOH	95	-14.135	46.511	18.743	1.00	37.17	1DIK3557
HETATM	3466	O	HOH	96	-4.814	10.202	6.231	1.00	37.24	1DIK3558
HETATM	3467	O	HOH	97	7.946	31.148	35.040	1.00	37.53	1DIK3559
HETATM	3468	O	HOH	98	-6.586	41.003	26.383	1.00	37.57	1DIK3560
HETATM	3469	O	HOH	99	-19.902	18.883	33.687	1.00	37.74	1DIK3561
HETATM	3470	O	HOH	100	-18.028	40.102	50.829	1.00	37.89	1DIK3562
HETATM	3471	O	HOH	101	-13.315	28.183	35.513	1.00	38.10	1DIK3563
HETATM	3472	O	HOH	102	-28.008	45.248	30.179	1.00	38.86	1DIK3564
HETATM	3473	O	HOH	103	0.486	39.943	46.308	1.00	39.11	1DIK3565
HETATM	3474	O	HOH	104	-2.576	4.959	28.921	1.00	39.13	1DIK3566
HETATM	3475	O	HOH	105	-25.042	47.163	37.757	1.00	39.65	1DIK3567
HETATM	3476	O	HOH	106	-13.645	35.978	48.302	1.00	40.20	1DIK3568
HETATM	3477	O	HOH	107	14.699	38.630	20.218	1.00	40.52	1DIK3569
HETATM	3478	O	HOH	108	-8.278	44.086	42.473	1.00	41.00	1DIK3570
HETATM	3479	O	HOH	1						

Figure 9

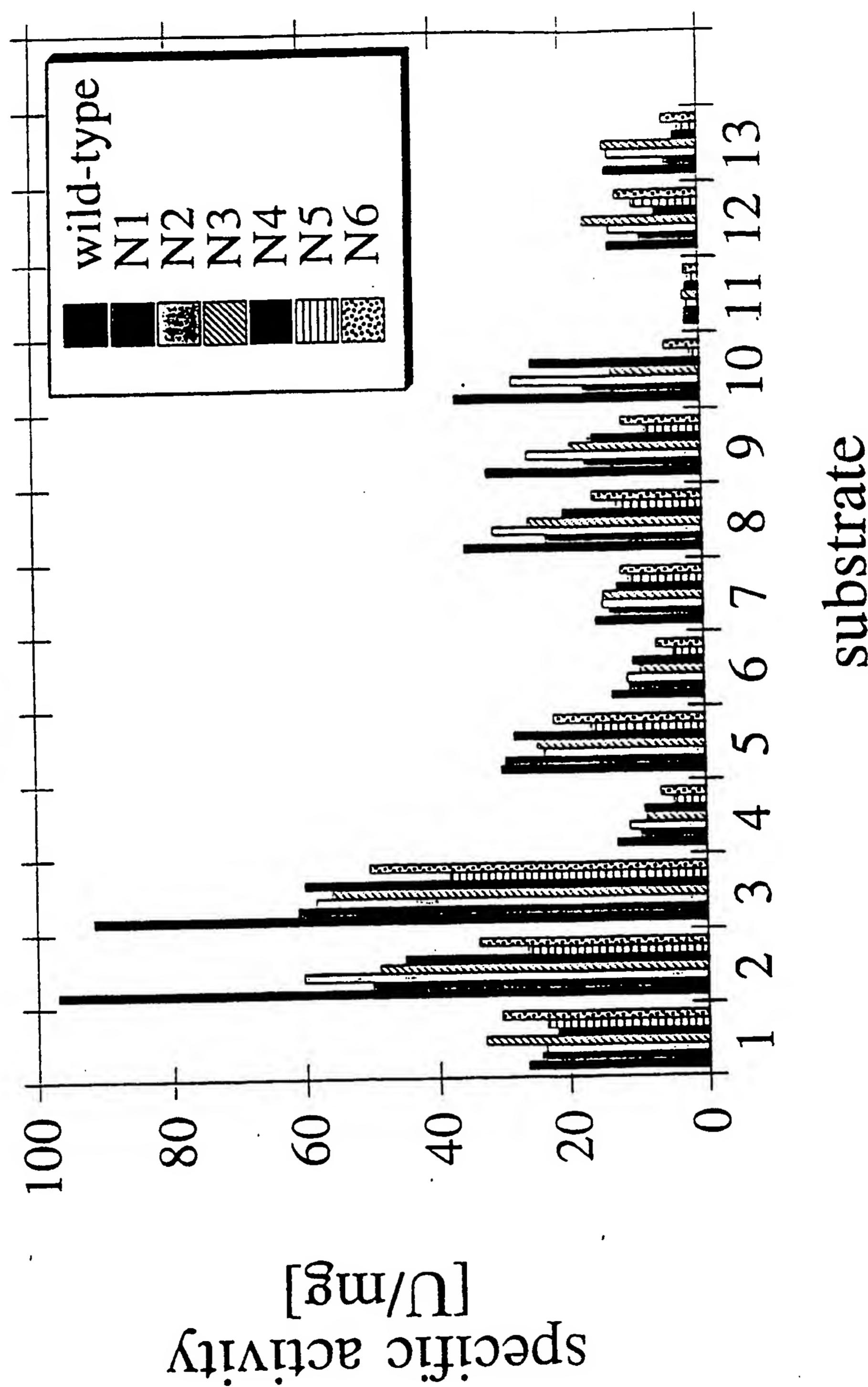
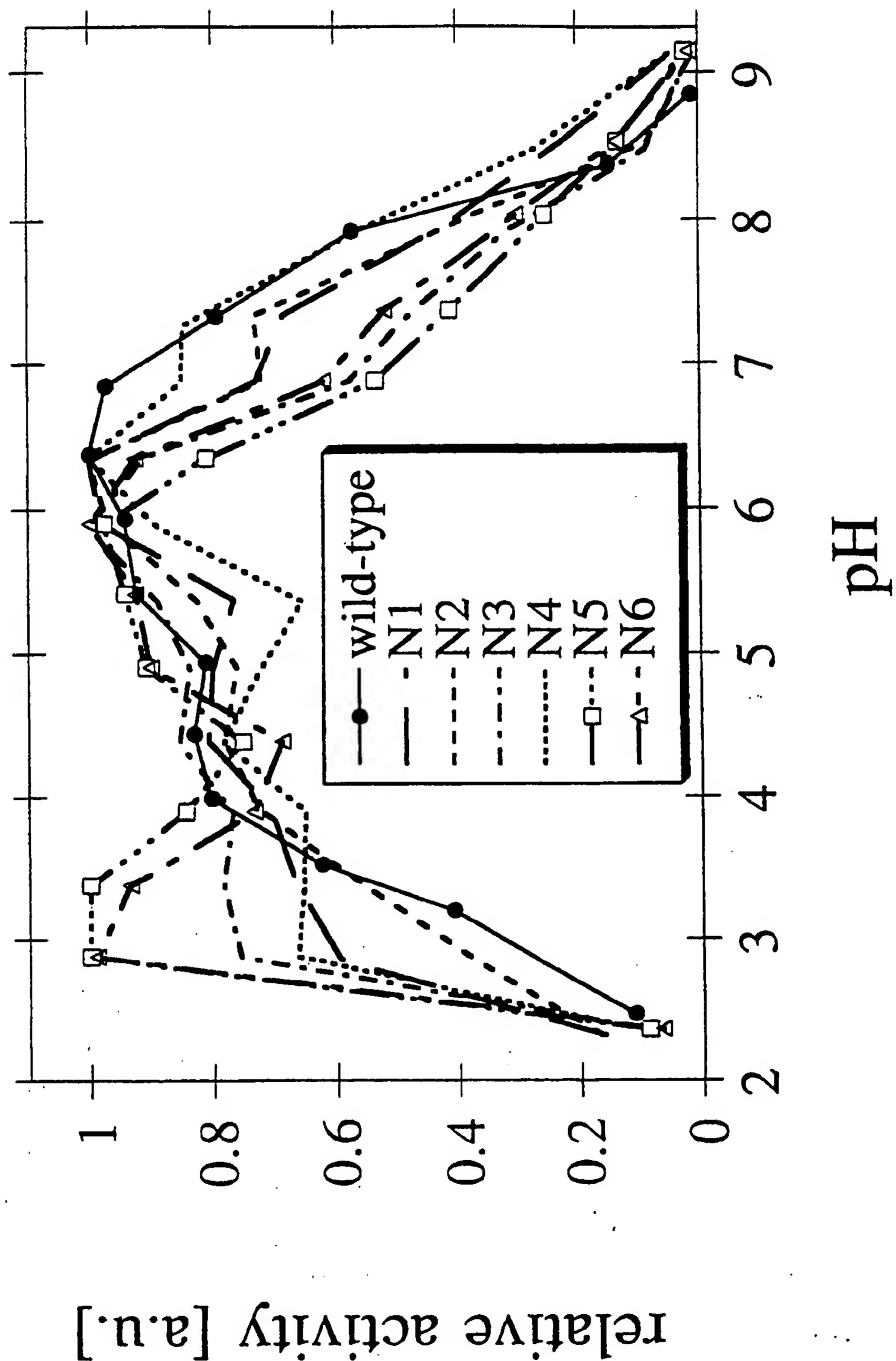


Figure 10



relative activity [a.u.]

Figure 11a



Figure 11b

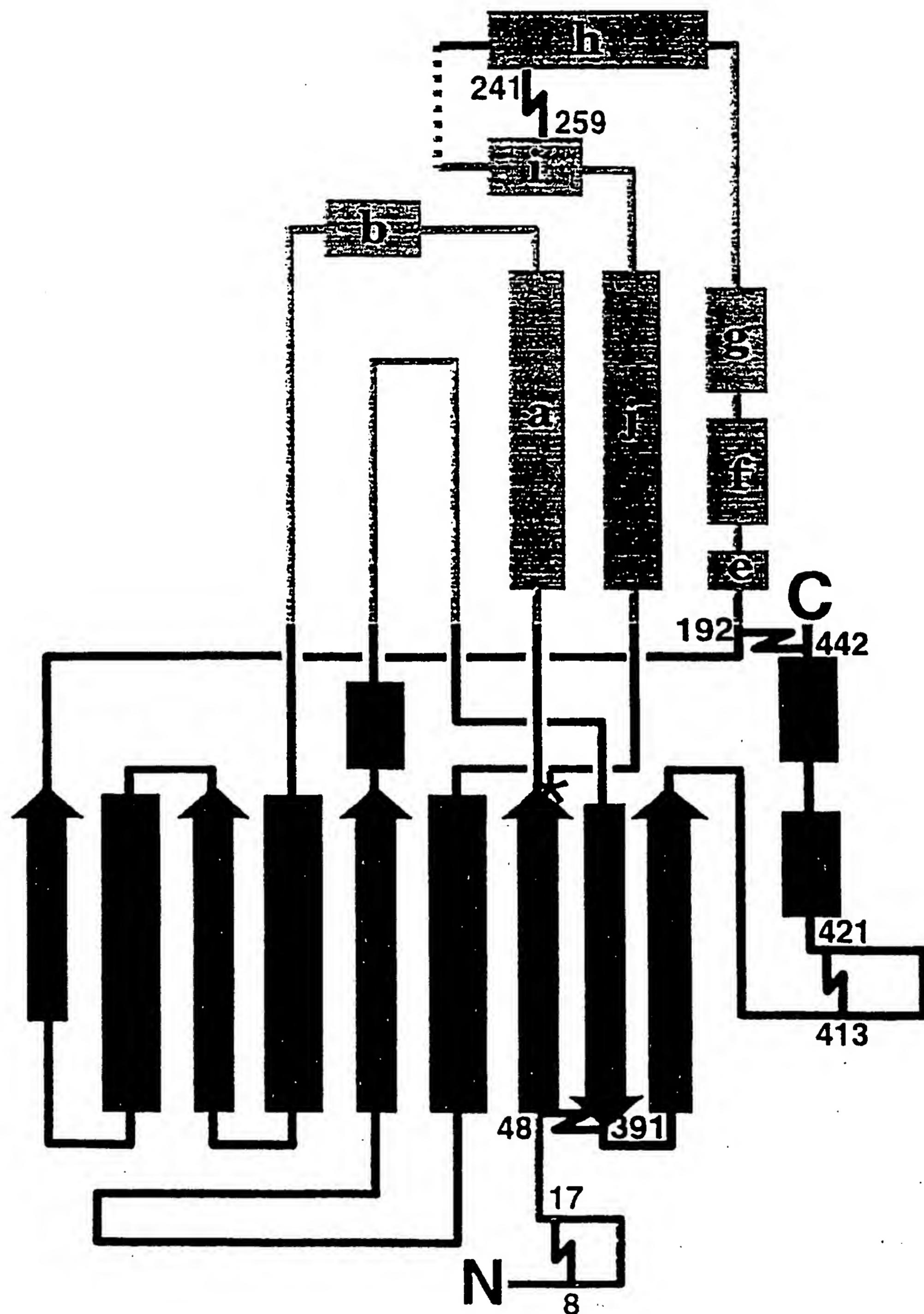
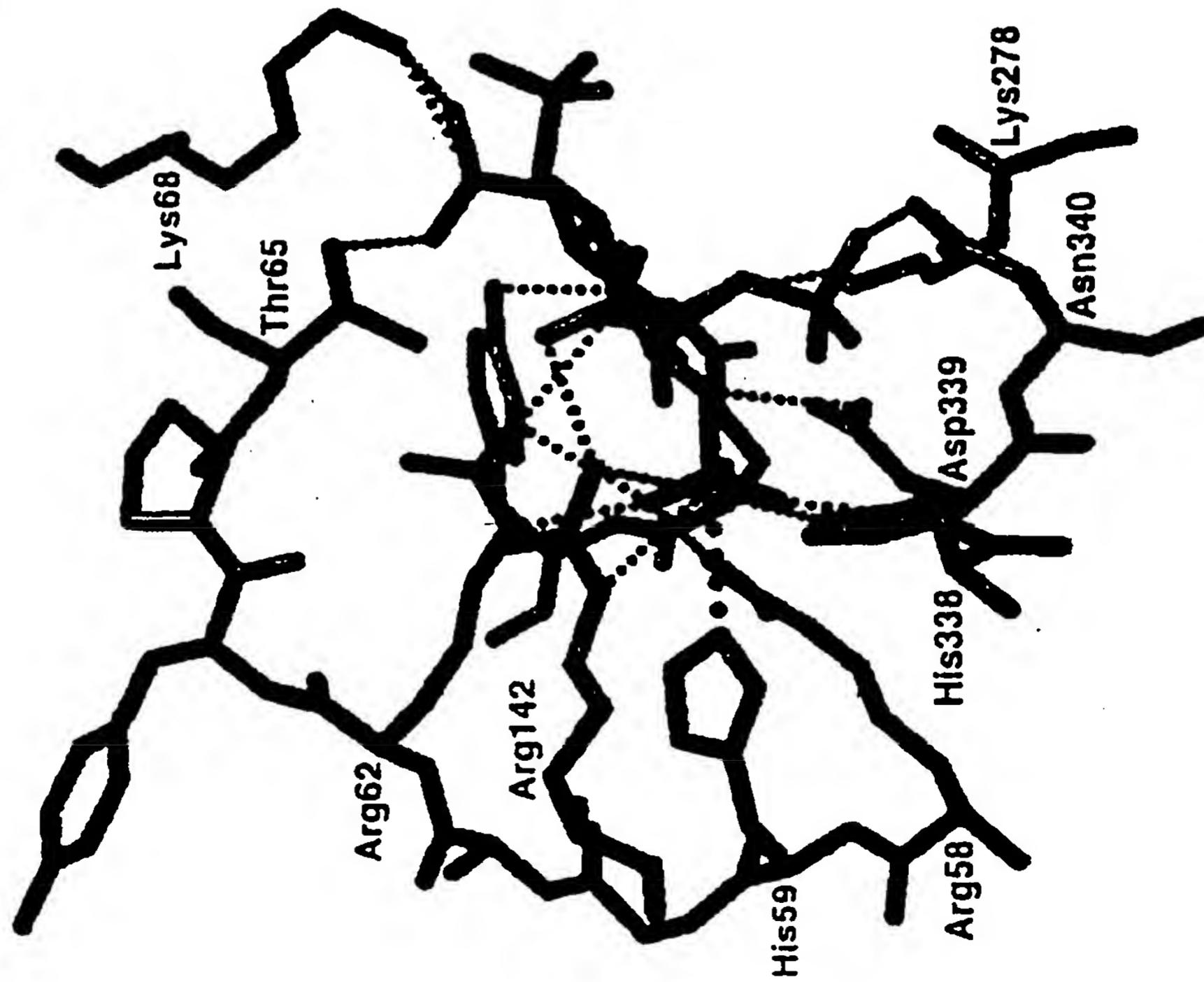
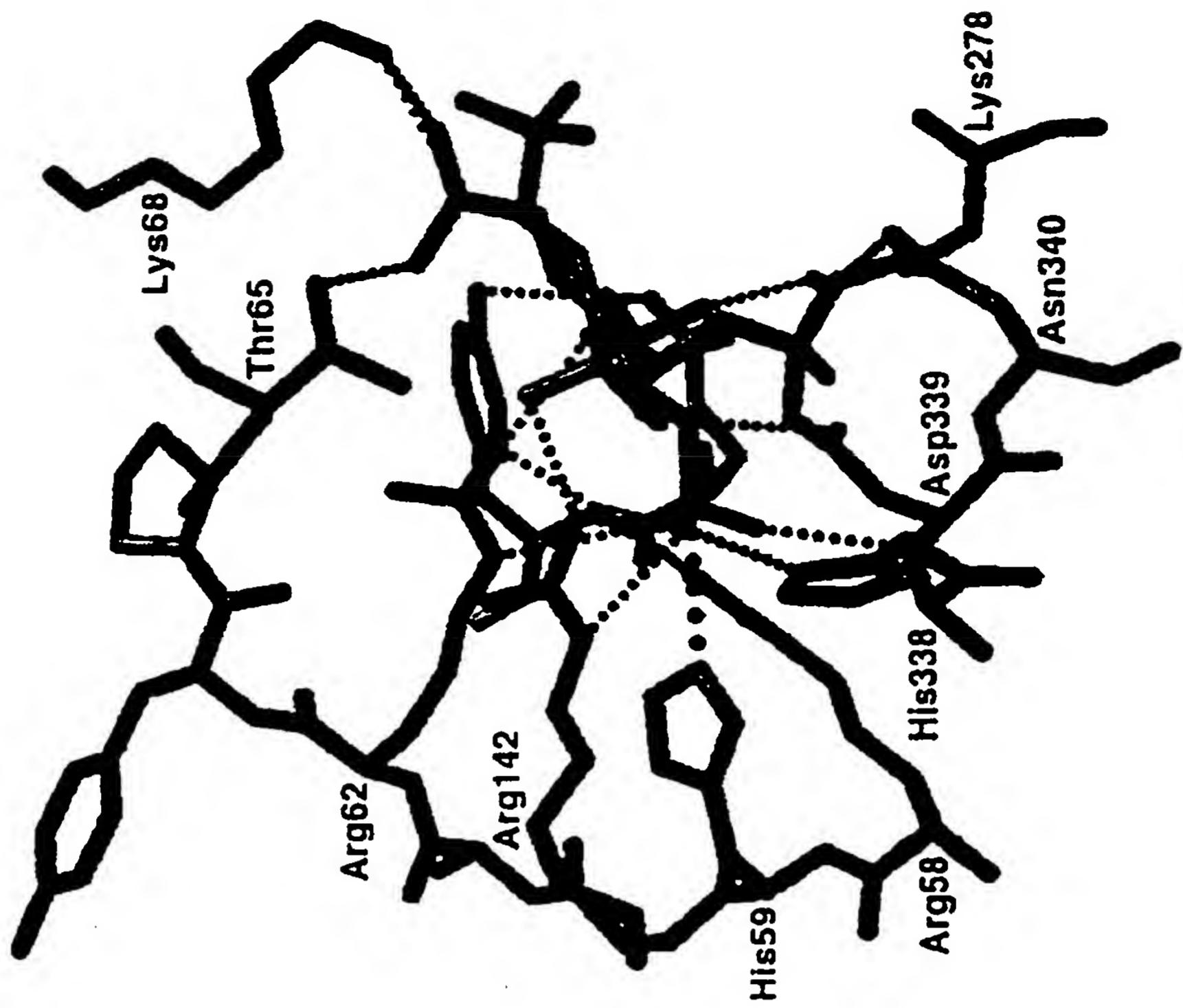


Figure 12



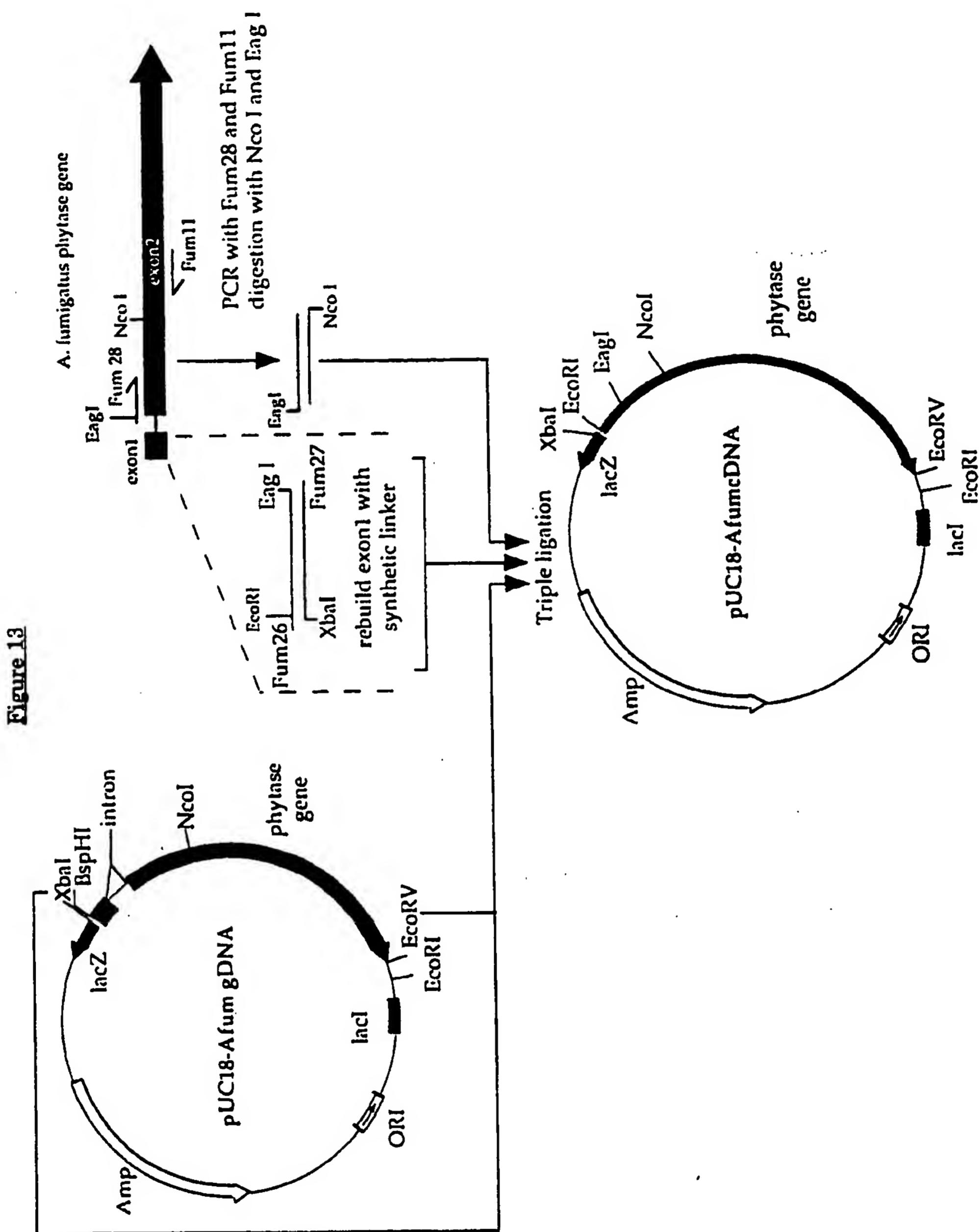


Figure 14a/1**Primer set A**

primer Q27L s	5'	CAT	CTA	TGG	GGC	<del>CTG</del>	TAC	TCG	CCA	TTC	3'
primer Q27L as	3'	GTA	GAT	ACC	CCG	GAC	ATG	AGC	GGT	AAG	5'
		H	L	W	G	<b>L<sub>27</sub></b>	Y	S	P	F	

**Primer set B**

primer Q274L s	5'	TAC	AAC	TAC	CTT	<del>CTG</del>	TCC	TTG	GGC	AAG	3'
primer Q274L as	3'	ATG	TTG	ATG	GAA	GAC	AGG	AAC	CCG	TTC	5'
		Y	N	Y	L	<b>L<sub>274</sub></b>	S	L	G	K	

**Primer set C**

primer G277D s	5'	CTT	CAG	TCC	TTG	GAC	AAG	TAC	TAC	GGC	3'
primer G277D as	3'	GAA	GTC	AGG	AAC	<del>CTG</del>	TTC	ATG	ATG	CCG	5'
		L	Q	S	L	<b>D<sub>277</sub></b>	K	Y	Y	G	

**Primer set D**

primer G277D* s	5'	CTT	CTG	TCC	TTG	GAC	AAG	TAC	TAC	GGC	3'
primer G277D* as	3'	GAA	GAC	AGG	AAC	<del>CTG</del>	TTC	ATG	ATG	CCG	5'
		L	<b>L<sub>274</sub></b>	S	L	<b>D<sub>277</sub></b>	K	Y	Y	G	

**Primer set E**

primer N340S s	5'	TTT	TCA	CAC	GAC	<del>AGC</del>	AGC	ATG	GTT	TCC	3'
primer N340S as	3'	AAA	AGT	GTG	CTG	<del>TCG</del>	TCG	TAC	CAA	AGG	5'
		F	S	H	D	<b>S<sub>340</sub></b>	S	M	V	I	

Figure 14a/2**Primer set F**

primer G277K s 5' C CTT CAG TCC TTG AAG AAG TAC TAC GGC TAC 3'  
 primer G277K as 3' G GAA GTC AGG AAC TTC TTC ATG ATG CCG ATG 5'  
                   L Q S L **K<sub>277</sub>** K Y Y G Y

**Primer set G**

primer A205E s 5' GGA GAT GAG GTT GAG GCC AAT TTC ACT G 3'  
 primer A205E as 3' CCT CTA CTC CAA CTC CGG TTA AAG TGA C 5'  
                   G D E V **E<sub>205</sub>** A N F T

**Primer set H**

primer Y282H s 5' AAG TAC TAC GGC CAC GGC GCA GGC AAC 3'  
 primer Y282H as 3' TTC ATG ATG CCG GTG CCG CGT CCG TTG 5'  
                   K Y Y G **H<sub>282</sub>** G A G N

**Primer set I**

primer AvrII s 5' GAT ACG GTA GAC CTA GGG TAC CAG TGC 3'  
 primer AvrII as 3' CTA TGC CAT CTG GAT CCC ATG GTC ACG 5'  
                   D T V D L G Y Q C

**Primer set J**

primer S66D s 5' CGG TAC CCA ACC GAT TCG AAG AGC AAA AAG 3'  
 primer S66D as 3' GCC ATG GGT TGG CTA AGC TTC TCG TTT TTC 5'  
                   R Y P T **D<sub>66</sub>** S K S K K

**Primer set K**

primer S140Y/D141G s 5' GC GCC TCA GGC TAC GGC CGG GTT ATT GC 3'  
 primer S140Y/D141G as 3' CG CGG AGT CCG ATG CGG GCC CAA TAA CG 5'  
                   A S G **Y<sub>140</sub>** **G<sub>141</sub>** R V I A

Figure 14a/3

**Primer set L**

primer S130N s    5'    CTG GCG CGC AAT GTG GTG CCG TTT ATT C    3'  
primer S130N as    3'    GAC CGC GCG TTA CAC CAC GGC AAA TAA G    5'  
                      L    A    R    **N<sub>130</sub>** V    V    P    F    I

**Primer set M**

primer R129L/S130N s    5'    GCT CTG GCG CTC AAT GTG GTG CCG TTT ATT C    3'  
primer R129L/S130N as    3'    CGA GAC CGC GAG TTA CAC CAC GGC AAA TAA G    5'  
                      A    L    A    **L<sub>129</sub>** **N<sub>130</sub>** V    V    P    F    I

**Primer set N**

primer K167G/R168Q s    5'    GAC CAT GGC TCC GGA CAA GCT ACG CCA G    3'  
primer K167G/R168Q as    3'    CTG GTA CCG AGG CCT GTT CGA TGC GGT C    5'  
                      D    H    G    S    **G<sub>167</sub>** **Q<sub>168</sub>** A    T    P

**Figure 14b**

**Primer set O**  
 FunG27-s 5' - CTA GGG TAC CAG TGC TCC CCT GCG ACT TCT CAT CTA TGG GCC **GGC** TAC TCG CCA TTC TTT TCG C - 3'  
 FunG27-as 3' - CC ATG GTC ACG AGG GGA CGC TGA AGA GTA GAT ACC CCG CCT ATG AGC GGT AAG AAA AGC GAG CT - 5'

**Primer set P**  
 FunV27-s 5' - CTA GGG TAC CAG TGC TCC CCT GCG ACT TCT CAT CTA TGG GCC **GTC** TAC TCG CCA TTC TTT TCG C - 3'  
 FunV27-as 3' - CC ATG GTC ACG AGG GGA CGC TGA AGA GTA GAT ACC CCG CAC ATG AGC GGT AAG AAA AGC GAG CT - 5'

**Primer set Q**  
 FunN27-s 5' - CTA GGG TAC CAG TGC TCC CCT GCG ACT TCT CAT CTA TGG GCC **AAC** TAC TCG CCA TTC TTT TCG C - 3'  
 FunN27-as 3' - CC ATG GTC ACG AGG GGA CGC TGA AGA GTA GAT ACC CCG **TTC** ATG AGC GGT AAG AAA AGC GAG CT - 5'

**Primer set R**  
 FunI27-s 5' - CTA GGG TAC CAG TGC TCC CCT GCG ACT TCT CAT CTA TGG GCC **ATC** TAC TCG CCA TTC TTT TCG C - 3'  
 FunI27-as 3' - CC ATG GTC ACG AGG GGA CGC TGA AGA GTA GAT ACC CCG **TAC** ATG AGC GGT AAG AAA AGC GAG CT - 5'

**Primer set S**  
 FunA27-s 5' - CTA GGG TAC CAG TGC TCC CCT GCG ACT TCT CAT CTA TGG GCC **GCG** TAC TCG CCA TTC TTT TCG C - 3'  
 FunA27-as 3' - CC ATG GTC ACG AGG GGA CGC TGA AGA GTA GAT ACC CCG **CAC** ATG AGC GGT AAG AAA AGC GAG CT - 5'

**Primer set T**  
 FunT27-s 5' - CTA GGG TAC CAG TGC TCC CCT GCG ACT TCT CAT CTA TGG GCC **ACG** TAC TCG CCA TTC TTT TCG C - 3'  
 FunT27-as 3' - CC ATG GTC ACG AGG GGA CGC TGA AGA GTA GAT ACC CCG **TGC** ATG AGC GGT AAG AAA AGC GAG CT - 5'

Figure 15:

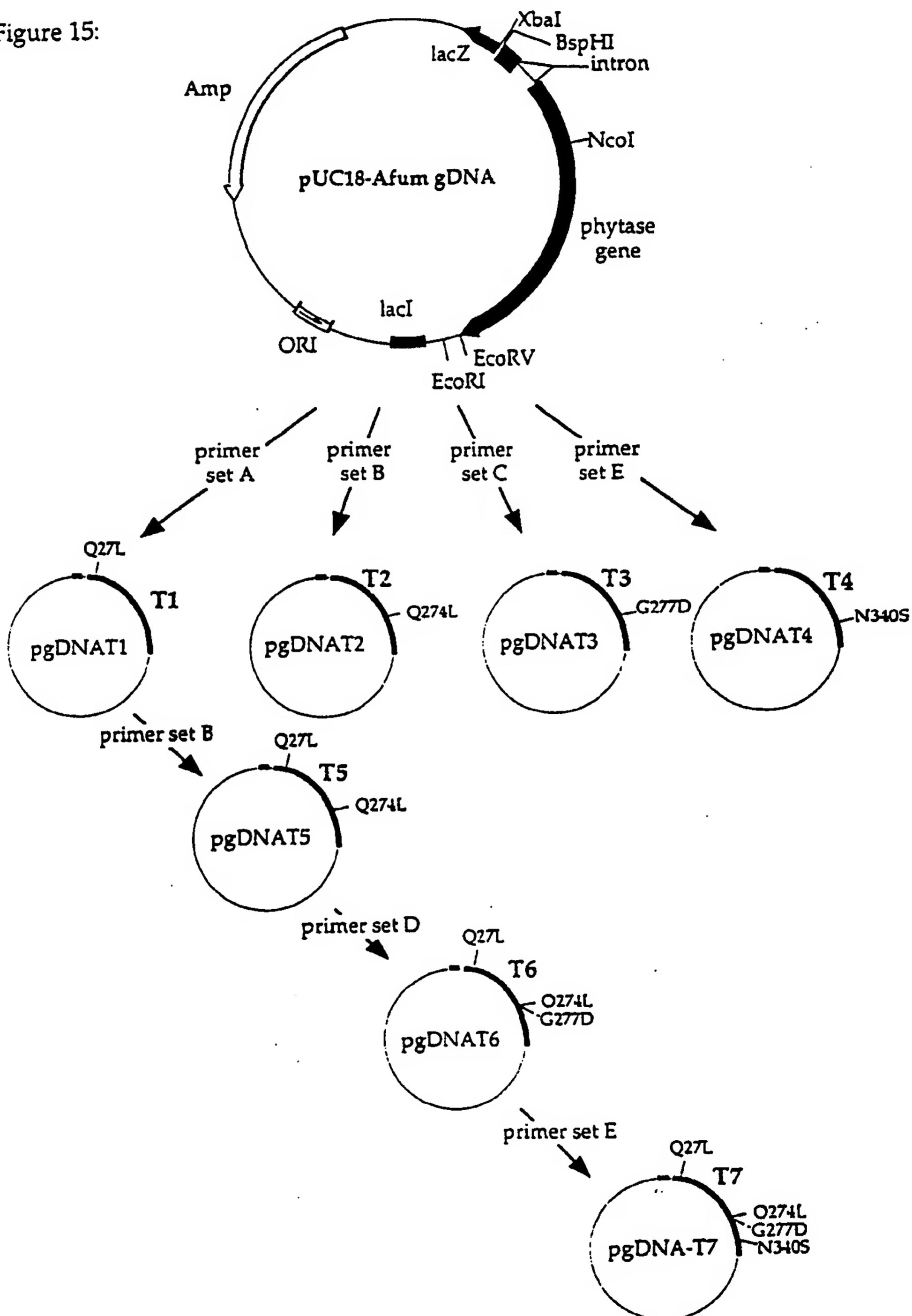


Figure 16:

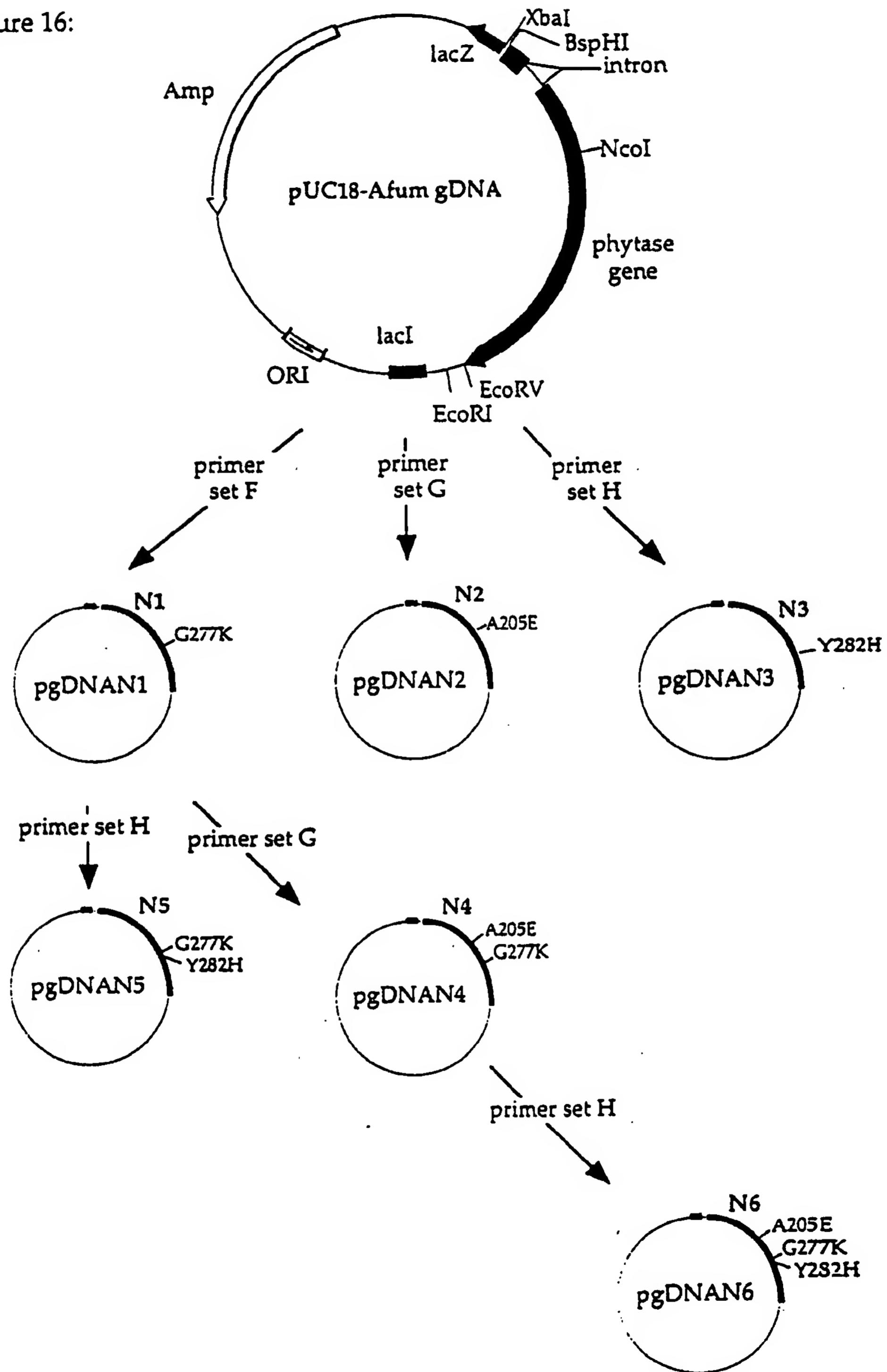


Figure 17a:

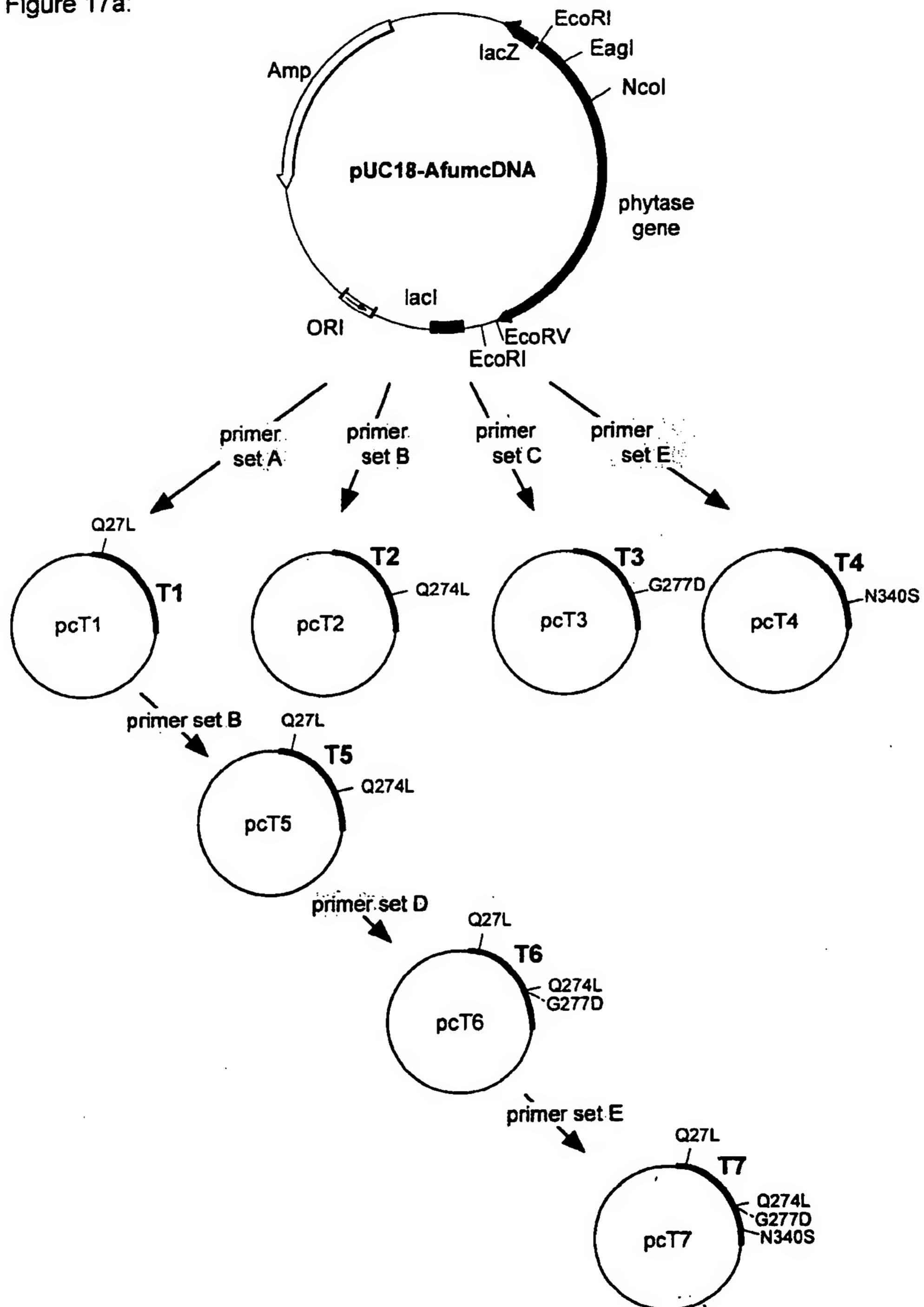


Figure 17b:

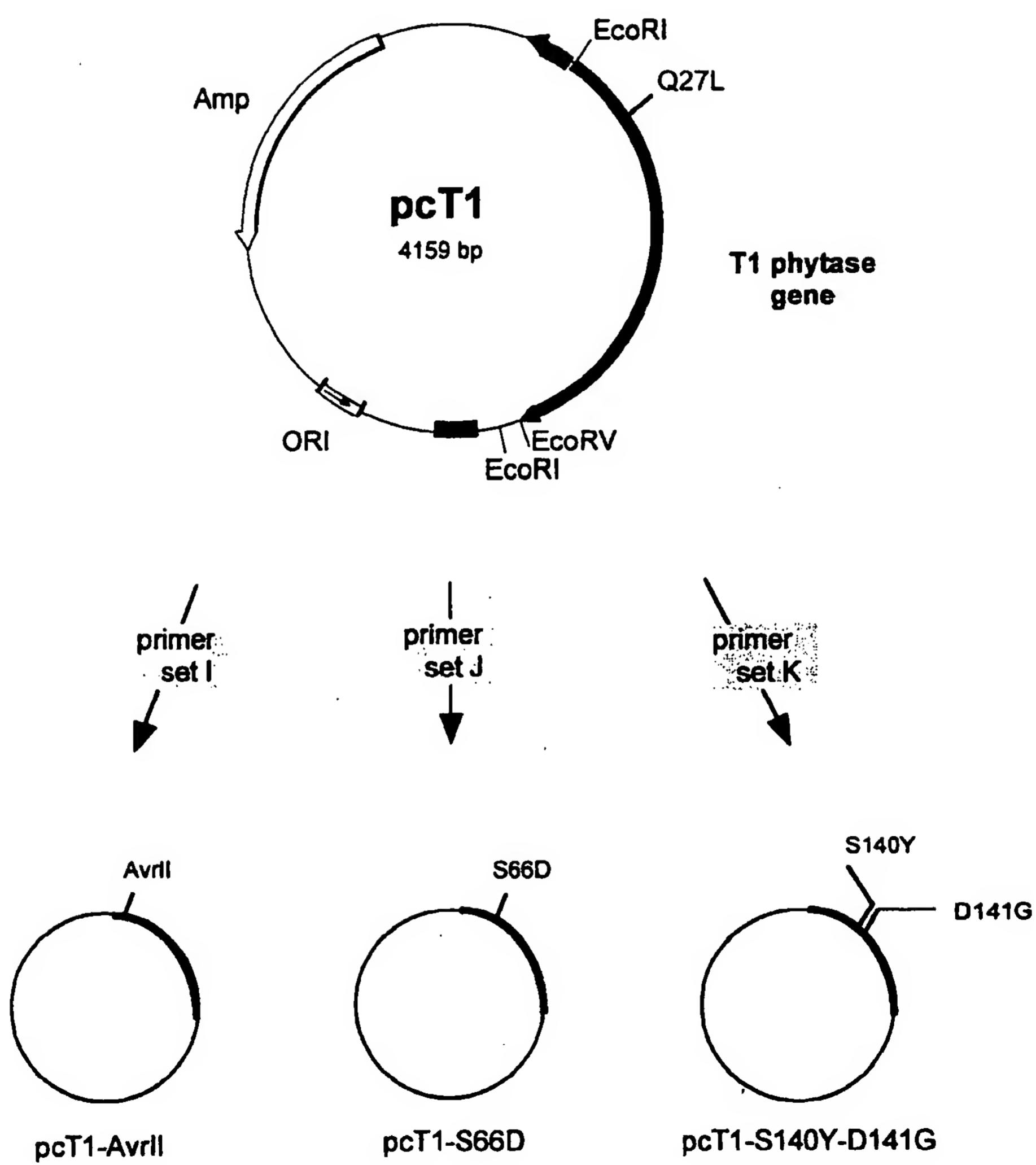


Figure 17c:

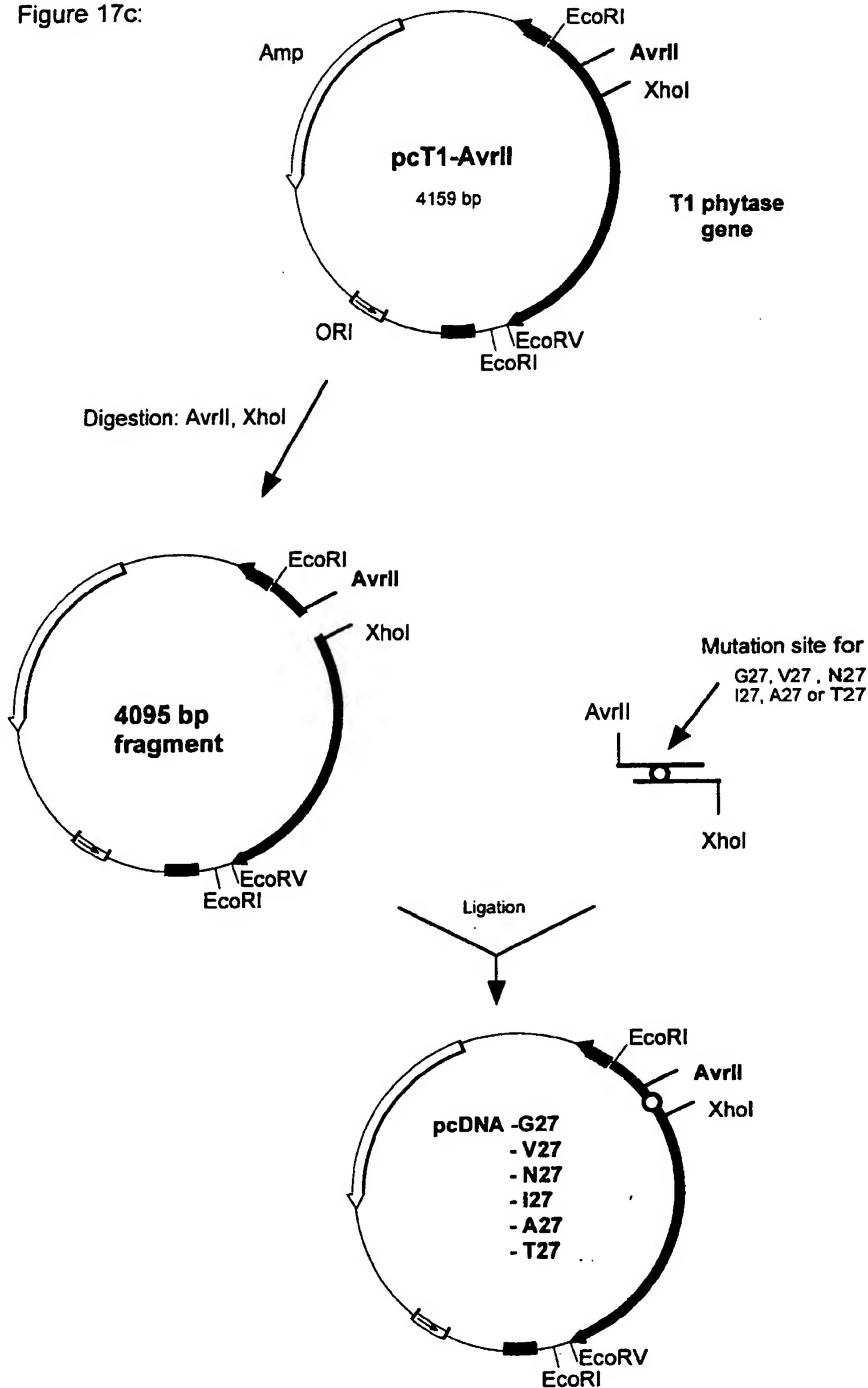


Figure 18:

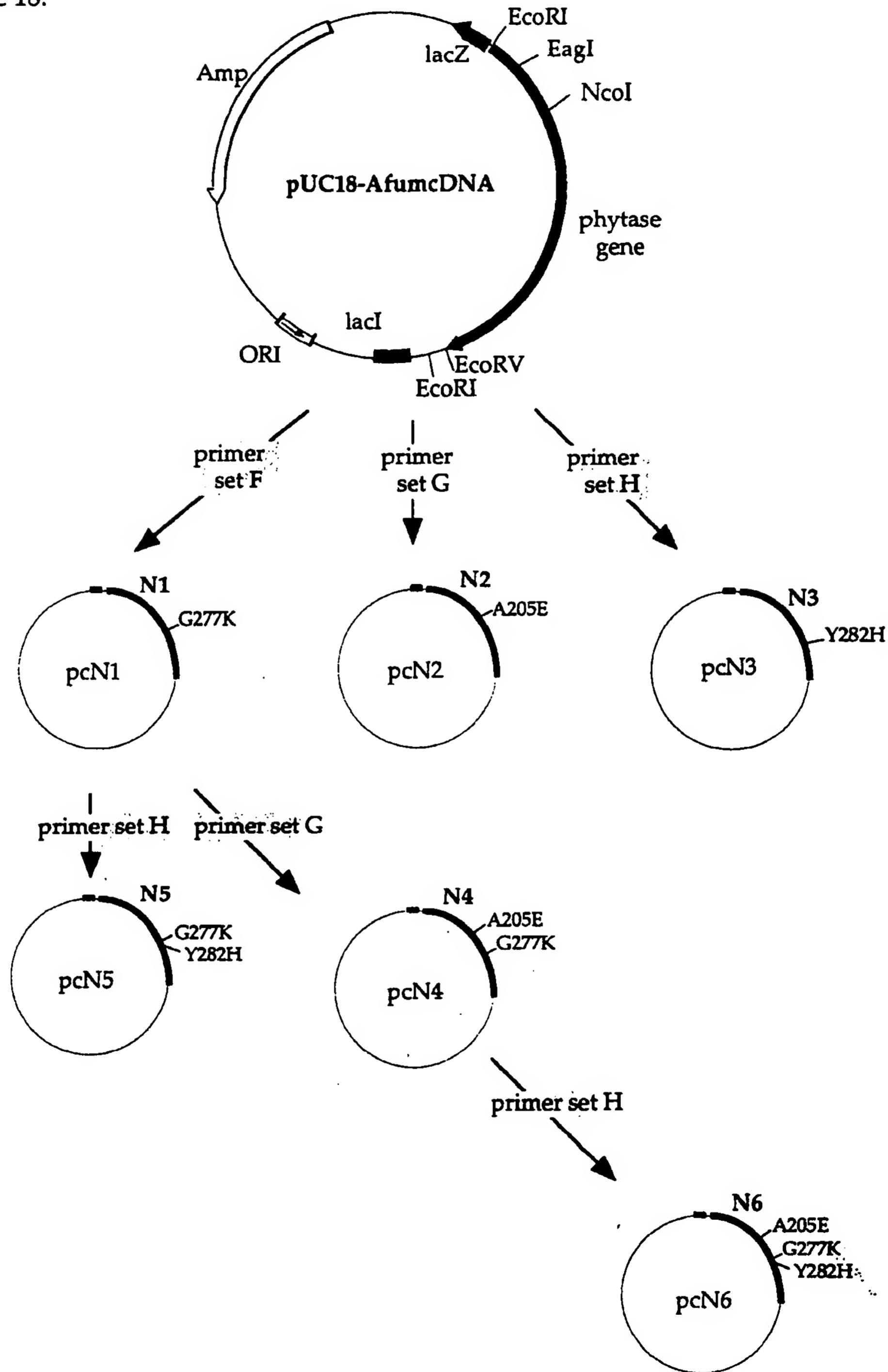
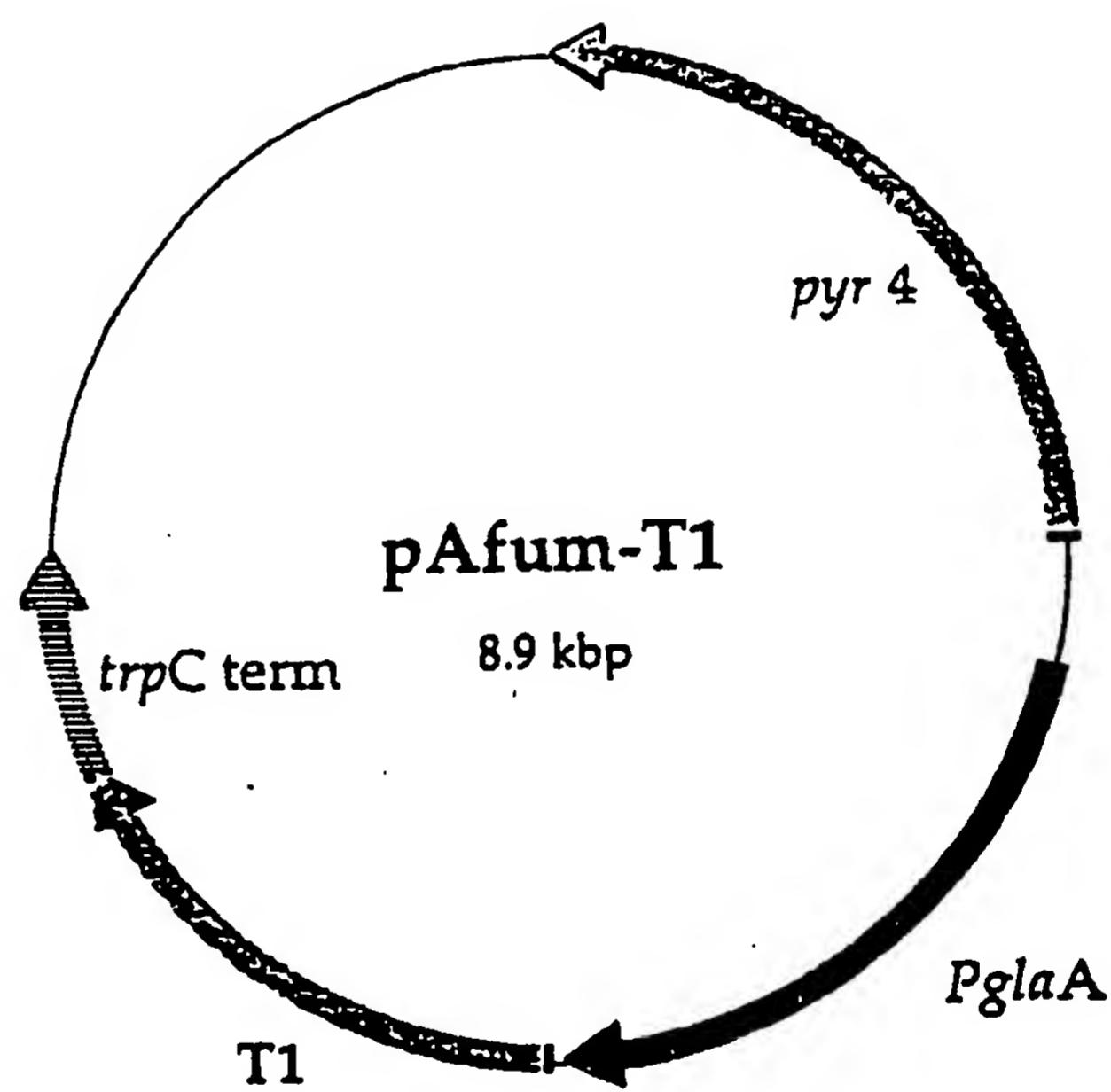


Figure 19:



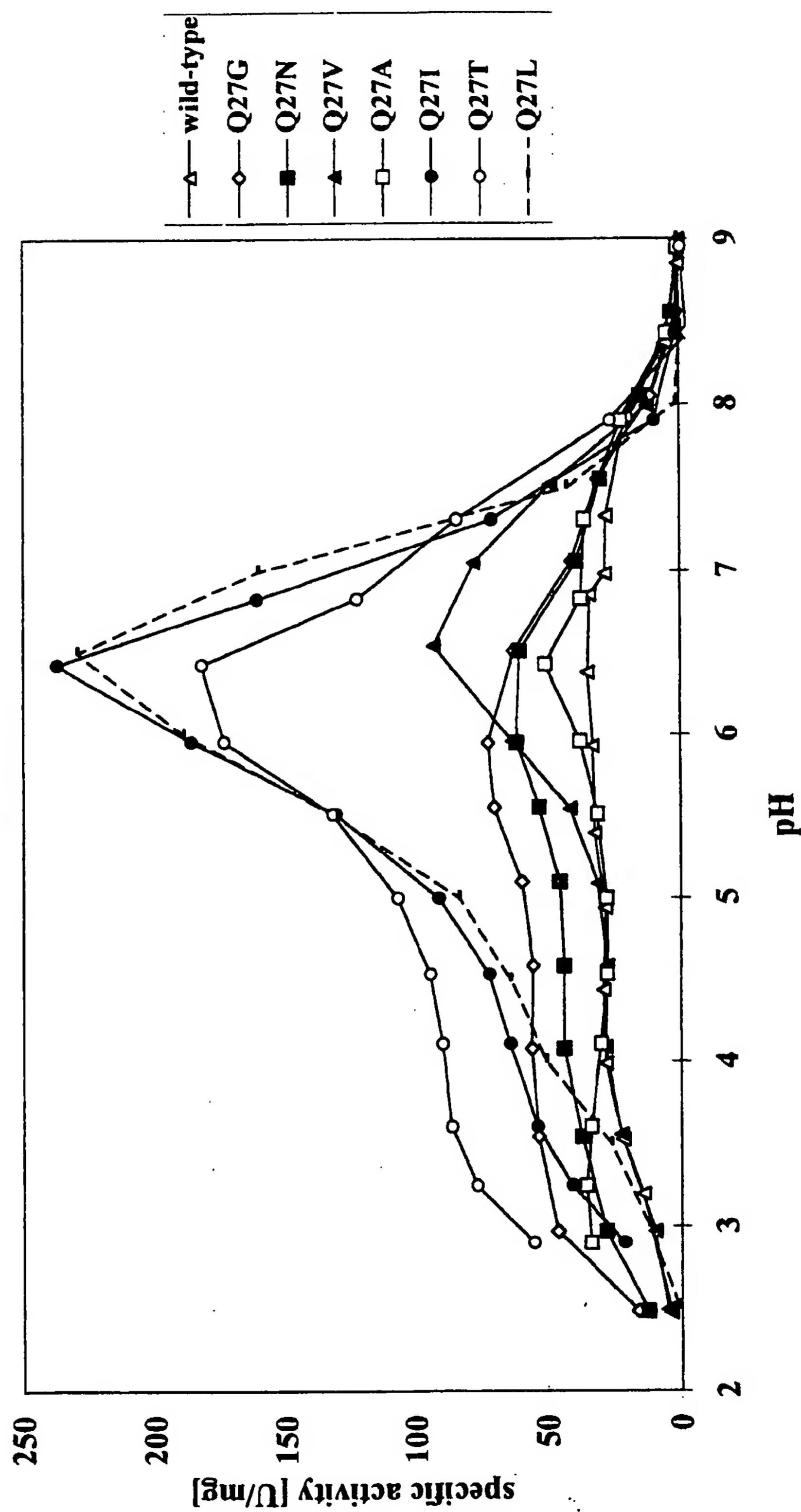
**Figure 20**

Figure 21

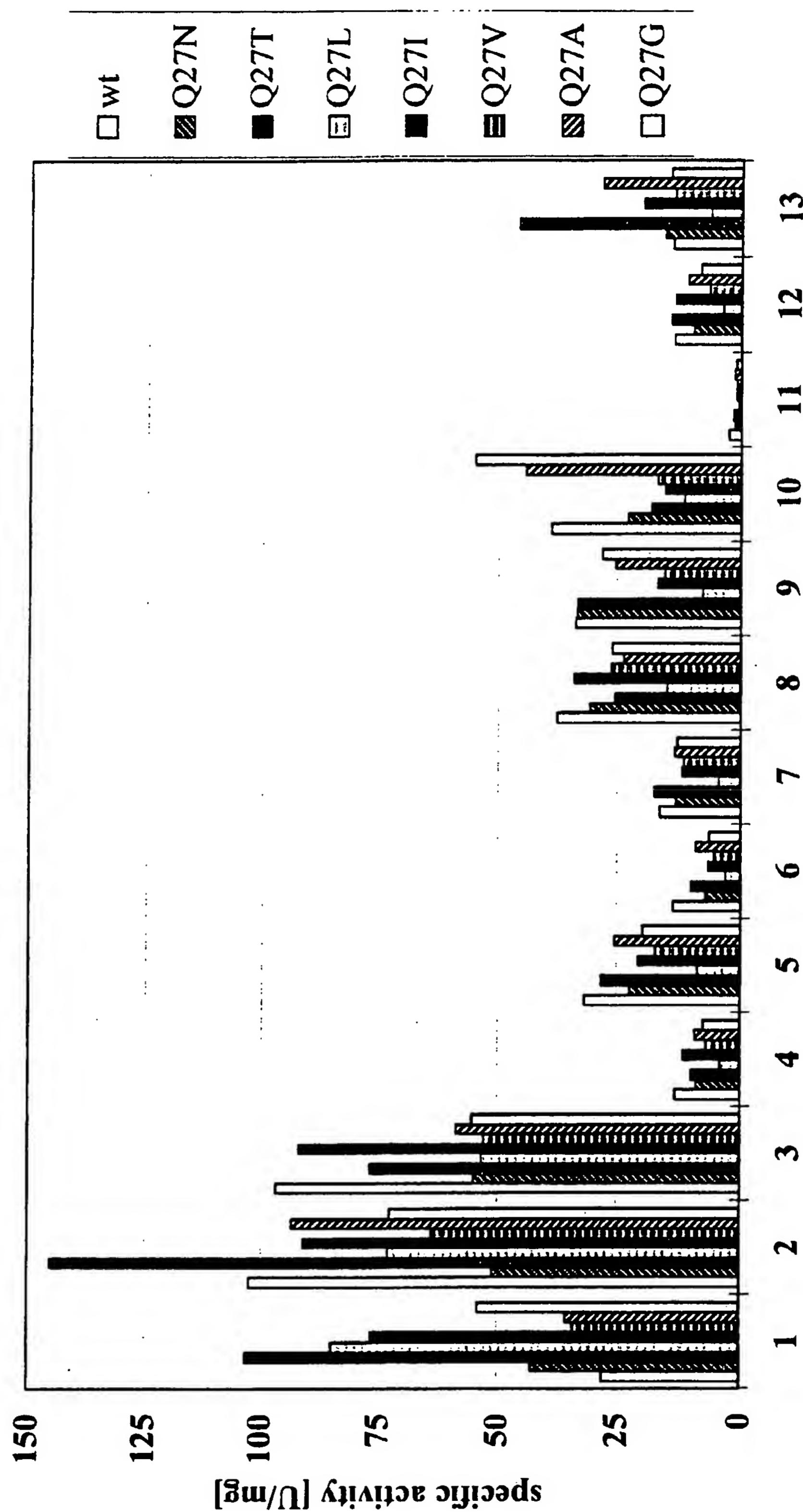


Figure 22

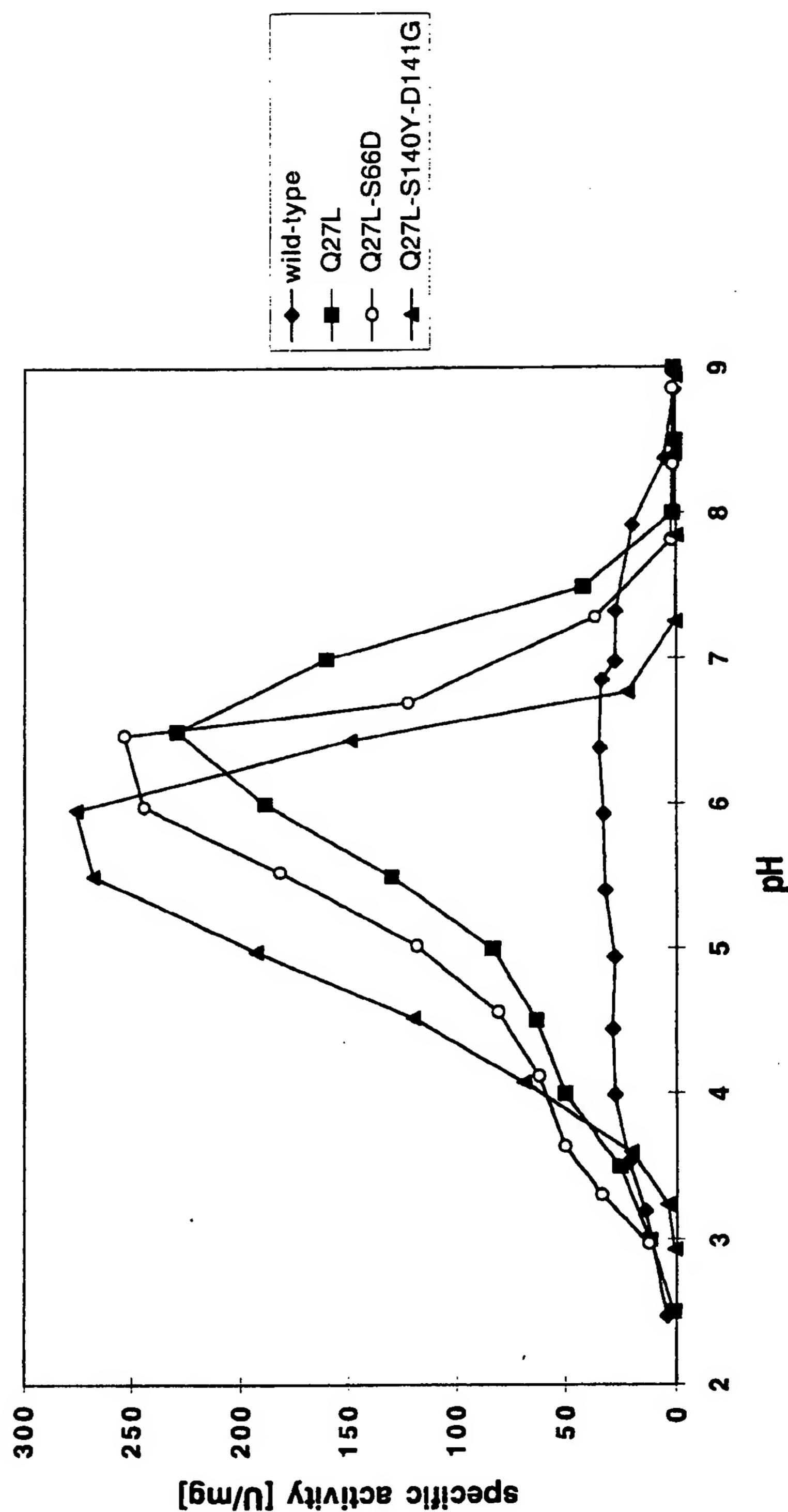
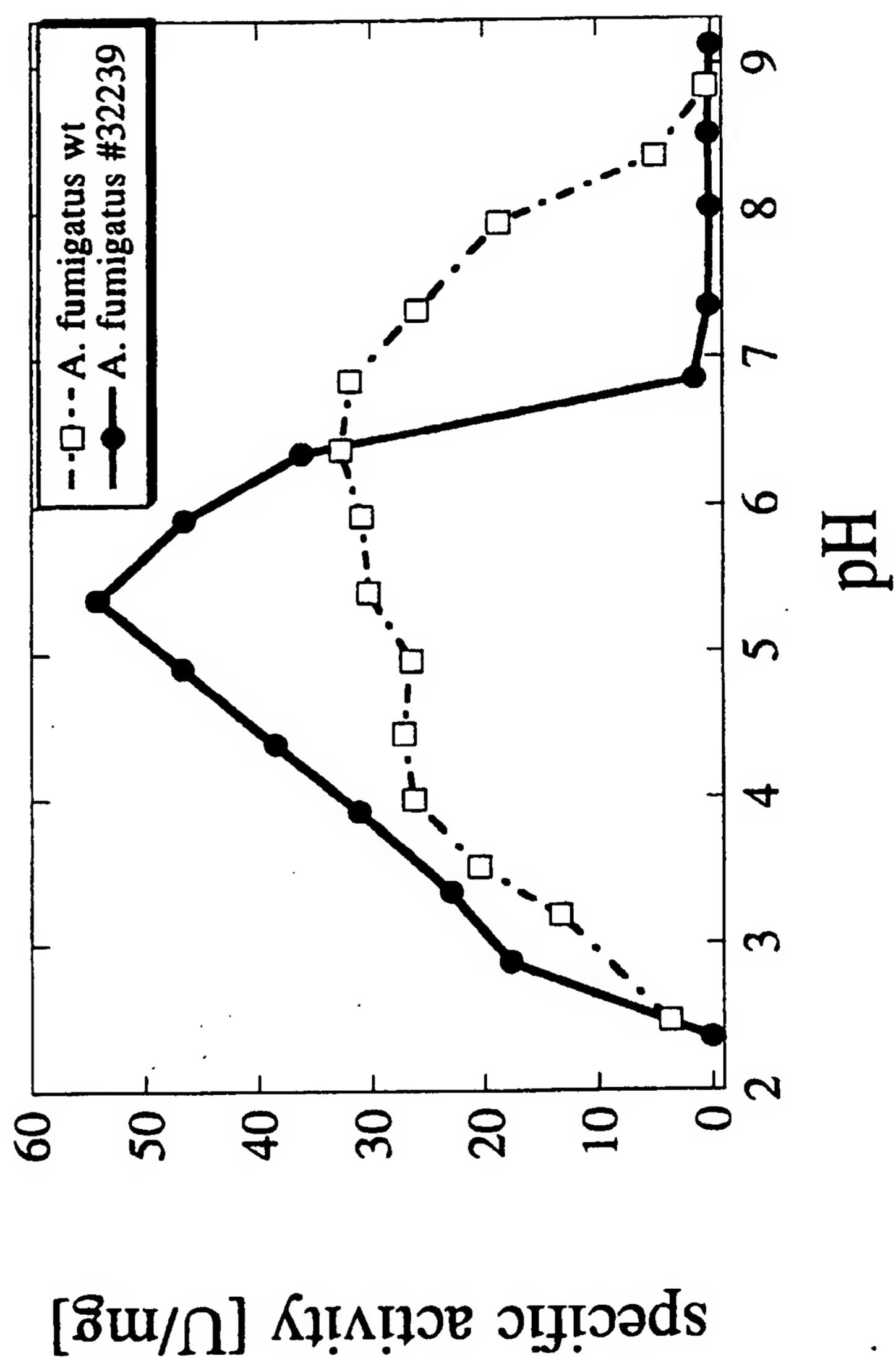


Fig. 23/1

1		#13073 MVTLTFLLSA NYLLSCRVSA APSS-----A CASKSCDTFVDL GYQCSPATSH LWGQYSPFFS LEPELSVSSK LPKDCRITLV #32722 ..... #58128 ..... #26906 ..... #32239 .GA..VH...AG...GCSAG ..A...E...Q...D...V.Y.	80
81	160	#13073 QVLSREGARY PTS8SKSKRYK KLVTAIQANA TDFKCKFATL KTISWYTLDAD DLTPFQEQQL VNSGCKPYQR YKAKLARGVVVP #32722 ..... #58128 ..... #26906 ..... #32239 ..... .....	160
161	240	#13073 PIRASESDRV IASCBKPIEG FQQQAKLA DPG ATNRMAPAS VILPESSETEN NTLDHGVCXK PHEASQLGDEV AANFTALFAP #32722 ..... #58128 ..... #26906 ..... #32239 ...S...N...E...V...Y... .....	240
241	320	#13073 DIRARAEKHL PGVTLTDEDV VSLNDHC BYD TVARTSDASQ LSPPFCQLPTH NWURKINYLQ SLCKYXYCQA GNPLCPAQGI #32722 ..... #58128 ..... #26906 ..... #32239 ..... .....	320

Fig. 23/2

400		
321	#13073	GFTNELLARL TRSPVQDHTS TWSTLVSNPA TTPLNATHYV DYSHDNSHVS IFFALGLYNG TEPLSLRTSVE BAKKLDGXYSA
	#32722	.....Q.....
	#58128	.....
	#26906	.....
	#32239	.....N.....D.D.....I.....Q.I.P.....T.E.....S.N.....
401		
470		
	#13073	BWVVPRAARA YFRTHQCKSE KEPPLVRALIN DRVVPPLHGCD DVVKLGRCKLN DVVKLGSLWAR SGCHNGCPS
	#32722	.....
	#58128	.....B.....
	#26906	.....
	#32239	.....
470		
		BB08

**Figure 24**

specific activity [U/mg]

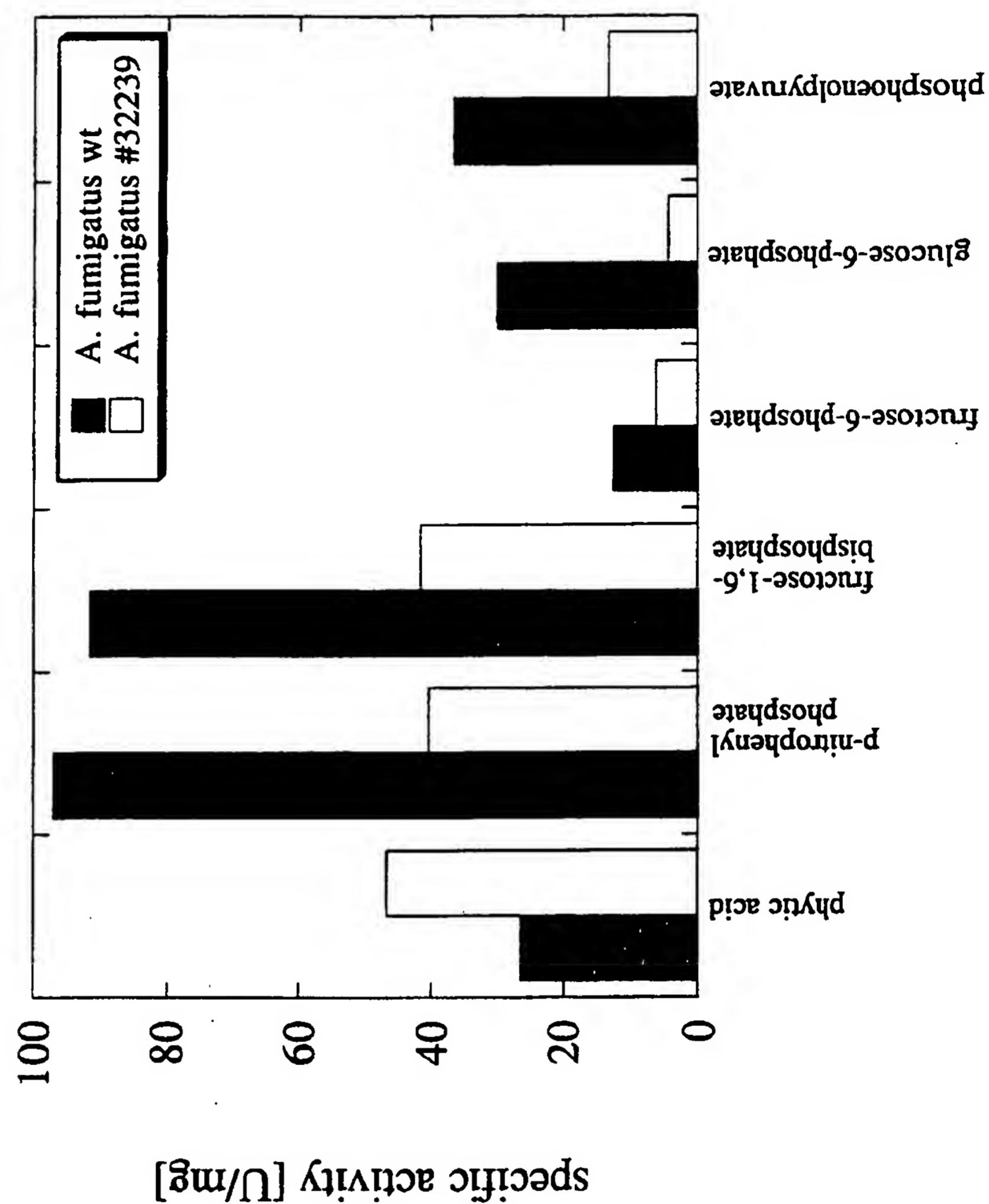
**Figure 25**

Figure 26:

